GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.

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OM nucleic - nu	OM nucleic - nucleic search, using sw model	
Run on:	April 8, 2003, 19:05:52 ; Search time 4068 Seconds (without alignments) 10444.960 Million cell updates/sec	
Title: Perfect score: Sequence:	US-09-595-947C-1 1460 1 gcaggtagcgagagcagagagtgacctaatccagtgt 1460	
Scoring table: OLIGO_NUC Gapop 60.0	OLIGO_NUC Gapop 60.0 , Gapext 60.0	

Total number of hits satisfying chosen parameters: Minimum DB seq length: 0 Maximum DB seq length: 2000000000

2054640 seqs, 14551402878 residues

Searched: Word size: 42842

Post-processing: Listing first 45 summaries

GenEmbl:*	gp_ba:*	gb_htg:*	dp_1n:*	gb_om:*	gb_ov:*	gb_pat:*	ap_ph:*	gb_pl:*	gb_pr:*	gb_ro:*	gb_sts:*	db_sy:*	ap_un:*	gb_v1:*	еш_ра:*	em finn:*
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score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	1167 Sequence 1 10619 R.norvegio 127817 Rattus no 76208 Mus muscu	364300 Mus musc 9167 M.musculus 09783 Mus muscu	Mus mu Homo s tion (4 Homo s Homo s	Human DN Human DN Homo sap Homo sap guence 4 us muscu	559 Gallus 66 M.muscul 11 Ms muscul 115 Sequenc 116 Gallus 77 Mus muscul 100 Gallus 100 Gallus 143 Mus mus 143 Mus mus 143 Mus mus 145 Mus	Y09596 Ggallus mR AR023709 Sequence U63842 Human neuro 184655 Sequence 10 AR023708 Sequence AR103242 Sequence BD000105 Different U58681 Homo sapien AF060885 Gallus ga BC008687 Homo sapien BC02826 Homo sapi BC02826 Homo sapi
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linear						ertebrata	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;			Icard-Liepkalns, C., Mallet, J. and Corresponding, N.A.	
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Submitted (20-JAN-1997) P. Ravassard, CNRS UMR 9923, Bat. CERVI.
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J. Neurosci. Res. 48 (2), 146-158 (1997)
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DCSARAGORGTSREIARARNGGRNERSKSELLERSKRANDRENRNRHNLNSA
LDALROVLPFPDARLTARETLERPHNYIMALTGTLRIADHSFVOFEPPPPGEGGS
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                                                /db_xref="taxon:10116"
/clone_lib="RT-PCR"
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*** SEQUENCING IN PROGRESS
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Sciurognathi; Muridae; Murinae;
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Muzny,D.M., Adams,C., Adio-Oduola,B.; Ali-osman,F.R., Allen,C., Alsoboks,S.L., Amaratunge,H.C., Are,J.R., Ayele,M., Banks,T., Barbaria,J., Benton,J., Bimage,K., Blankenburg,K., Bonnin,D., Bouck,J., Bowie,S., Brieva,M., Brown,E., Brown,M., Bryant,N.P., Buhay,C., Burch,P., Burkett,C., Burrell,K.L., Byrd,N.C.,
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N Rattus norvegicus clone CH230-259G16, ***
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contig of 1639 bp in length gap of unknown length contig of 1407 bp in length contig of 1930 bp in length gap of unknown length gap of unknown length gap of unknown length gap of unknown length contig of 1744 bp in length
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Carron, T.F., Carter, M., Cavazos, S.R., Chacko, J., Chavez, D., Chen, R., Chen, R., Chowdhry, I., Christopoulos, C., Chen, R., Chen, R., Chowdhry, I., Christopoulos, C., Cavaland, C.D., Cox. C., Coyle, M.D., Dathorne, S.R., David, R., Davila, M.L., Davis, C., Davy, Carroll, L., Dederich, D.A., Davis, C., Davis, C., Dan, A.L., Dhog, Y., Dinh, H.H., Douthwaite, K.J., Draper, H., Dugan-Rocha, S., Durbin, K.J., Frantz, P., Falls, T., Ferragutco, D., Flagg, M., Ford, J., Esotto, M., Falls, T., Ferragutco, D., Riagg, M., Ford, J., Foster, P., Frantz, P., Gabisi, A., Gao, J., Garcia, A., Garner, T., Hale, S., Hamilton, K., Harris, C., Harris, K., Harris, K., Harris, C., House, J., Garcia, A., Garner, P., Hale, S., Hamilton, K., Harnandez, O., Hodgson, R., Housey, M., Hollews, M., Hallis, B., Homai, F., Howard, S., Huber, J., Hulyk, S., Hume, J., Jackson, L.E., Jackson, E., Katisson, E., Karisson, E., Marking, M., Marting, M., M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

NOTE: This is a 'working draft' sequence. It currently consists of 80 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the flnished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Direct Submission
Submitted (19-JUL-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          center clone name: CH30-259G16
Sequencing vector: Plasmid;
Chamistry: Dye-terminator Big Dye: 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality; 73194 bases at least Q40
Consensus quality: 79767 bases at least Q30
Consensus quality: 84278 bases at least Q20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
------ Project Information
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2 (bases 1 to 166677)
Worley, K.C.
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2147
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JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL
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COMMENT

ROD 05-FEB-1997

us-09-595-947c-1.rge

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/translation-"MAPHPLDALTIQVSPETQQPFPGASDHEVLSSNSTPPSPTLIPR
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PGGGGNGWGSTSPYSOGRNLSPFASLEEFPGLQVPSSPSYLLPGALVFSDFL"
274 c 250 g 155 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              l (bases 1 to 861)
Sommerii. Mai.O. and Anderson, D.J.
neurogenins, a novel family of atonal-related bHiH transcription
factors, are putative mammalian neuronal determination genes that
reveal progenitor cell heterogeneity in the developing CNS and PNS
Mol. Cell. Neurosci. 8 (4), 221-241 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musimus
1 (bases 1 to 861)
                                                                                                                                                            58181 GITGGGAGACTCCCATACTTCCTGGTGACTCCGCCCTCTTTCAAATCTGCGGGCCTCCAA 58240
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Sommer,L., Ma.Q. and Anderson,D.J.
Direct Submission
Submitted (24-0CT-1996) Biology 216-76, California Institute of
Technology, Howard Hughes Medical Institute, Pasadena, CA 91125,
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                            TCCTCAGTGTGGCCACCTCAAACTCCCGCTCCAAGCAGAGGAGGAGGCCGTAGCACTAAATA
                                                    GTTGGGAGACTCCCATACTTCCTGGTGACTCCGCCCCTTTTCAAATCTGCGGGCCTCCAA
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Location/Qualifiers
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100.0%; Pred. No.
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/protein_id-"AAC53029.1"
/db_xref-"GI:1666912"
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/gene="ngn3"
160. .804
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Direct Submission
Submitted (01-AUG-2000) Lemaigre F.P., Hormone and Metabolic
Research Unit, Louvain University Medical School, Avenue Hippocrate
75, box 7529, Brussels 1200, BELGIUM
On oct 31, 2000 this sequence version replaced g1:1666087.
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DCSEARYGDCRGTSRKLRARRGGRNRPKSELALSKQRRSRRKKANDRERNRMHNLNSA
LDALRGVLPTFPDDAKLTKIETLRFAHNYIMALTQTLRIADHSFYGPEPPVPCGELGS
PGGGSNGDWGSIYSPYSQAGNLSPTASLEEFPGLQVPSSPSYLLPGALVFSDFL"
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Jacquemin,P., Durviaux,S.M., Jensen,J., Godfraind,C., Gradwohl,G., Guillemot,F., Madsen,O.D., Carmeliet,P., Dewerchin,M., Collen,D., Rousseau,G.G. and Lemaigre,F.P.
Transcription factor hepatocyte nuclear factor 6 regulates parcreatic endocrine cell differentiation and controls expression of the proendocrine gene ngn3
MOI. Cell. Biol. 20 (12), 4445-4454 (2000)
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                                                                                                                                                                                                                                              Direct Submission
Submitted (04-NOV-1996) G.J. Gradwohl, IGBMC,
CNRS-INSERM-Universite Louis Pasteur, BP163, C.U. de Strasbourg,
F-67404 ILLKIRCH cedex, FRANCE
Revised by [4]
4 (bases 1 to 5567)
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/strain="SV129"
/db_xraf="taxon:10090"
/clone="lambda GEM12 clone 19C"
/cell_line="D3"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /translation-"MAPHPLDALTIQVSPETQQPFPQASDHEVLSSNSTPPSPTLIPR
DCSEAEVGCRGTSRKLRARGGRRRPKSELALSKORRSRRKKANDRERNRHINLNSA
LDALRGVLPTPPDDDAKLTKIETLRFAHNYIWALTQTLRIADHSFYGPEPPVPCGELGS
PGGGSNGOWGSIYSYGANLESEFPGLQVPSSPSYLLPGALVFSDFL"
560 c 537 g 367 t
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                                                                                                                                                                                                           Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostoml;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 1861)
Lee,J., Smith,S., Watada,H., Lin,J., Scheel,D., Wang,J., Mirmira,R. and German,M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                 ROD 03-MAY-2001
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Cau,E., Gradwohl,G., Fode,C. and Guillemot,F.
Mashi activates a cascade of bHLH regulators in olfactory neuron
                                                                                                                                                                                                                                                                                                                                  Regulation of the pancreatic pro-endocrine gene neurogening Diabetes (2001) In press
2 (bases I to 1861)
Schwitzgebel, v. and German, M.
Direct Submission
Submitted (26-MAR-2001) Hormone Research Institute, University of California San Francisco, 513 Parnassus Ave, HSW1090, San Francisco, CA 94145-0534, USA
Location/Qualifiers
1 .1861
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1396 GCGCTGGATGCGCTGCGCGGTGTCCTGCCCACCTTCCCGGATGACGCCAAACTTACAAAG 1455
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llarity 100.0%; Pred. No. 1.5e-42;
Conservative 0; Mismatches 0;
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/protein_id-"AAK50058.1"
/db_xref-"GI:13937129"
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1093, .1737
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                                                                                 AF364300 1861 bp
Mus musculus neurogenin 3 gene,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /db_xref="taxon:10090"
<1093: .>1737
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Matches
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PUBMED
REFERENCE
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ACCESSION VERSION KEYWORDS SOURCE JOURNAL

us-09-595-947c-1.rge

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AC127417 185806 bp DNA linear HTG 15-JUL-2002 Mus musculus chromosome UNK clone RP23-459M2, WORKING DRAFT SEQUENCE, 36 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 185806) and Waterston, R.H.

The sequence of Mus musculus clone Unpublished

2 (bases 1 to 185806)

McPherson, J.D. and Waterston, R.H.

McPherson, J.D. and Waterston, R.H.

Direct Submission

Submitted (15-JuL-2002) Genome Sequencing Center, 4444 Forest Park Parkway, St. Louis, MO 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                   Db 110917 GGGCTGGATGCGCTGCGGGGTGTCCTGCCCACCTTCCCGGATGACGCCAAACTTACAAAG 110858
                                                                                                                                                                                                                                                                                                                                               762 GCGCTGGATGCGCTGCGCGGTGTCCTGCCCACCTTCCCGGATGACGCCAAACTTACAAAG 821
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Center code: WUGSC
                                                                                                                                                                                                                                                              Length 138070;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Quality coverage: 3.66 in Q20 bases; agarose-fp Quality coverage: 3.85 in Q20 bases; sum-of-contigs
                                    bp in length
length
bp in length.
                                                                                                                                                                                                     1425 others
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chemistry: Dye-primer ET; 0% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 173518 bases at least Q30
Consensus quality: 177276 bases at least Q30
Consensus quality: 179611 bases at least Q20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Web site:http://genome.wustl.edu/gsc/index.shtml
Contact: submissions@watson.wustl.edu
                                                                                                                                                                                                                                             DB 2; Lens.
                     length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               132682: contig of 4354 by
132770: gap of unknown 14
136341: contig of 3571 by
136429: gap tig unknown 14
138070: contig of 1641 by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Db 110857 ArcgAGACCCTGCGCTTCGCCCACAACTACAT 110826
                                                                                                                                                                                                     35731 a 33657 c 33303 g 33954 t
                                                                                                                                                                                                                                                              6.3%; Score 92; DB 100.0%; Pred. No. 1.2 iive 0; Mismatches
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                                                                                                                                          /organism-"Mus musculus"
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Sequencing vector: plasmid; 100%
                                                                                                                                                             /db_xref="taxon:10090"
/clone="RP23-121F10"
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HTG; HTGS_PHASE1; HTGS_DRAFT.
                                                                                                 Location/Qualifiers
1. .138070
                                                                                                                                                                                                                                                              Query Match 6.3
Best Local Similarity 100.
Matches 92; Conservative
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                                        132771
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KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (07-FEB-2002) Lita Annenberg Hazen Genome Sequencing Center, Cold Spring Harbor Laboratory, 1 Bungtown Road, Cold Spring Harbor, NY 11724, USA
                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. I (bases 1 to 138070)
MCCOmbie, W.R., Basker, J.P., Ballja, V., Dedhia, N.N., de la Bastide, M., Katzenberger, F., Kult, K., King, L., Kirchoff, K.A., Miller, B., Muller, S., Nascimento, L.U., O'Shaughnessy, A.L., Preston, R.R., Santos, L., Spiegel, L.A., Palmer, L., Yang, C. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Center: Lita Annenberg Hazen Genome Center, Cold Spring Harbor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            * NOTE: This is a 'working draft' sequence. It currently consists of 17 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
    Mus musculus clone RP23-121F10, WORKING DRAFT SEQUENCE, 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Insert size: 173000; sum-of-contigs
Insert size: 141616; sum-of-contigs
Quality coverage: 4.00 in Q20 bases; agarose-fp
Quality coverage: 3.70 in Q20 bases; sum-of-contigs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: mccombie@cshl.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Web site: http://www.cshl.org/genseq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             unknown
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                                                             AC109783.1 GI:18581594
HTG; HTGS_PHASE1; HTGS_DRAFT.
Mus musculus.
Mus musculus
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                                                                                                                                                                                                                                                                                                     Mouse Genomic Sequence Unpublished
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162443: gap of unknown length
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  arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be todated with the finished sequence as soon as it is available and the accession number will be preserved.
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Continuation (4 of 4) of AC079846 from base 300001 (AC079846 Homo sapiens chromosome
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Homo sapiens BAC clone RP11-402J6 from 4, complete sequence.
AC023886
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Submitted (15-MAR-2002) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St.
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Radionenko,M. and Abbott,A.
The sequence of Homo sapiens BAC clone RP11-402J6
Upublished (2001)
(bases 1 to 179697)
Waterston,R.H.
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Contact: sapiens@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                           DD 86995 AAGATCGAGACCCTGCGCTTCGCCCACAACTACAT 86961
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Genome Res. 8 (11), 1097-1108 (1998)
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Submitted (18-FEB-2000) Genome
University School of Medicine,
MO 63108, USA
4 (bases 1 to 179697)
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Mammalia; Eutheria; Primates;
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MHNINAALDALREVLPTFPEDAKLTKIETLRRAHNTWALTETLRLADHCGGGGGGLP
GALFSRAVLLSPGGASAALSSGGDSPSPASTWSCTNSPAPSSSVSSNSTSPYSCTLSP
ASPAGSDMDVWQPPEDKHRYAPHLEIARDCI"
1536 c 1507 g 1596 t
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                                                                                                                                                                                                                                                                                              Db 159127 GCGCTGCATGCGCTGCCCGGTGTCCTGCCCACCTTCCCGGATGACGCCAAACTTACAAAG 159186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 6123)
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Neurogenin2 expression in ventral and dorsal spinal neural tube
progenitor cells is regulated by distinct enhancers
Dev. Biol. 229 (2), 327-339 (2001)
                                                                                                                                                                                                                                                           762 GCGCTGGATGCGCTGCGCGGTGTCCTGCCCACCTTCCCGGATGACGCCCAAACTTACAAAG 821
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                                                                                                                                                                             Length 185806;
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Simmons, A.D., Horton, S., Abney, A.L. and Johnson, J.E.
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Homo sapiens neurogenin 2 gene, partial cds.
AF303002
                                                                                                                                                                             DB 2; Le
1.2e-42;
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                                                                             /note="assembly_name:Cont1g57"
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139099: 149579
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                                                                                                                                                                             6.3%; Score 92; DB 100.0%; Pred. No. 1.2 tive 0; Mismatches
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Best Local Similarity
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Best Local Similarity
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TITLE
JOURNAL
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Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.

Sequencing Center, Washington 4444 Forest Park Parkway, St. Louis,

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This sequence may not represent the entire insert of this It may be shorter because we only sequence overlapping
Center project name: H_NH0402J06
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Gaps

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Indels

819 AAGATCGAGACCCTGCGCTTCGCCCACAACTACAT 853

63108, USA

Louis,

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6833. 36848
'note="match to EST AI537116 (NID:94451251) to15h09.x1"
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                                                                                                                                                                                                         Mapping information for this clone was provided by Dr. John D. McPherson, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see http://genome.wustl.edu/gsc.
                                                  This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >-30); an attempt was made to resolve all sequencing problems, such as compressions and repeats, all regions were covered by sequence from more than one subclone; and the assembly was confirmed by
                                                                                                                                                                                                                                                                                                             The RPCI-11 human BAC library was made from the blood of one male donor, as described by Oscegawa. X., Woon, P.Y., Zhao, B., Frengen, E. Tateno, M., Catanese, J.J. and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8 "The Clone may be obtained either from Research Genetics, Inc. (http://www.resgen.com) or Pleter de Jong and coworkers at http://www.chori.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The clone sequenced to the left is AC004049, 2000 bp overlap; the clone sequenced to the right is RP11-148B6. Actual end of this clone is at base position 179697 of RP11-402J6.
clone sections once, or longer because we provide a small overlap between neighboring data submissions.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism-"Homo sapiens'
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PRI 19-0CT-2001

RESULT 12 HSA133776 LOCUS DEFINITION

ACCESSION VERSION KEYWORDS SOURCE ORGANISM

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/translation-"MTPQPSGAPTVQVTRETERSFPRASEDEVTCPTSAPPSPTRTRG
NCARREDGCGRAPRILRARRGGRSRPKSELALSKORRSRRKKANDRERNRMINILNSA
LADALRCVLPTPSDDAKLTKIETLRFAHNTWALTQTLRIADHSLYALEPPAPHCGELG
SPGGSPPGDMSLYSQAGGSLSPRAALEERPGLLGATSSACLSPGSLAFSDFL"
1500 c 1514 g 1111 t
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                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. (pases I to 5340) del Bosque-Plata, L., Lin, J., Horikawa, Y., Schwarz, P.E., Cox, N.J., Iwasaki, N., Ogata, M., Iwamoto, Y., German, M.S. and Bell, G.I. Mutations in the coding region of the neurogenin 3 gene (NEUROG3) are not a common cause of maturity-onset diabetes of the young in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 165110)
Howden,P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 (bases 1 to 5340)
Lin.J. and German.M.
Direct Submission
Submitted (15.FEB-2000) Hormone Research Institute, University o
California San Francisco, 513 Parnassus Ave., San Francisco, CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 5340;
                                                                                                                                       AF234829 5340 bp DNA linear
Homo sapiens neurogenin 3 gene, complete cds.
AF234829
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llarity 100.0%; Pred. No. 1e-06;
Conservative 0; Mismatches 0
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                                       535 AAGAGCGAGTTGGCACTGAGCAAGCAGCGACG 566
                 AAGAGCGAGTTGGCACTGAGCAAGCAGCGACG 703
                                                                                                                                                                                                                                                                                                                                                                                                                   Japanese subjects
Diabetes 50 (3), 694-696 (2001)
21140923
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Matches 32; Conserv
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Human DNA
sequence.
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LOCUS
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AUTHORS
                   672
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JOURNAL
                                                                                                                 RESULT 13
AF234829
LOCUS
                                                                                                                                                                                          ACCESSION
VERSION
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MEDLINE
PUBMED
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KEYWORDS
SOURCE
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NCARREGGGGAPRKLRARRGGRSRPKSELALSKORRSRRKKANDRERNRMHDLNSA
LDALRGVLPTFPDDAKLTRIETLRFAHNTIWALTQTLRIADHSLYALEPPAPHCGELG
SPGGPPGDWGSLXSVGGSLSPAASLEERPGLLGATSSACLSPGSLAFSDFL"
459 c 413 g 228 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The human neurogenin 3 homolog maps to chromosome 10q21.3 and its expression pattern is identical to that of its murine counterparts Unpublished
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Submitted (16-MAR-1999) Ravassard P., Lgn, CNRS UMRC 9923, Hopital
de la Pitie Salpetriere, Bat. CERVI, 83 Bd. de 1'Hopital, 75013
PARIS, FRANCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Euteleostomi;
/rpt_family="Alu"
39941. .40230
/rpt_family="Alu"
39941. .39956
/note="match to EST AA775240 (NID:92834574) ad18a05.s1"
40767. .40798
                                                                                                                                                                                                                                                                                                                                                                                                     AJ133776.1 GI:5123782
DHLH transcription factor; neurogenesis; neurogenin 3; ngn3 gene
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Ravassard, P., Icard-Liepkalns, C., Wiard, L., Julien, J.P. and
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                                                                                                                                     Length 179697;
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae,
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Best Local Similarity 100.0%; Pred. No. 1.1e-06;
Matches 32; Conservative 0; Mismatches 0;
                                                                                                                                                                         0
                                                                                                                                 Query Match 2.4%; Score 35; DB 9; L. Best Local Similarity 100.0%; Pred. No. 1.4e-08; Matches 35; Conservative 0; Mismatches 0;
                                                                                                                                                                                                          /function-"early neurogenesis"
                                                                                                                                                                                                                                                                                                                                                  DNA
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/gene="ngn3"
                                                                                                                                                                                                                                                                                                                                                               Homo sapiens gene for neurogenin 3. AJ133776
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /protein_id="CAB45384.1"
/db_xref="GI:5123783"
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/db_xref="taxon:9606"
1 1330
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322. .966
/gene="ngn3"
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/gene="ngn3"
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Ravassard, P.
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FEATURES

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AUTHORS

TITLE

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BASE COUNT ORIGIN

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Jane 1. 1888 repeat: matches 2. .114 of consensus" 17719. .18069 footset: matches 7617. .7977 of consensus" 18117. .181345 footse matches 7. .262 of consensus" footse MIR repeat: matches 7. .262 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="LiPA15 repeat: matches 5480. .6157 of consensus" 38265. .38561
                                                                                                                                                                                                                                                                                                                                                                                                                                              .7917 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20738, 20773
/note="UZ repeat: matches 1. 36 of consensus"
20802, 20863
/note="MILIT repeat: matches 1. .62 of consensus"
20889, 21263
/note="MILIF repeat: matches 188. .541 of consensus"
21633, 21618
/note="WIL repeat: matches 46. .192 of consensus"
22019, 22336
/note="MILIF repeat: matches 10. .306 of consensus"
20019, 22336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22381. .22564
/note="L2 repeat: matches 2453. .2629 of consensus"
22896. .23174
/note="MLTIJ repeat: matches 117. .413 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23215. .23346

//oote="MIR repeat: matches 48. .188 of consensus"

23388. .23532

23531. .23837

//oote="123837 //oote="1303 of consensus"

//oote="AluJb repeat: matches 1. .303 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23838. .24137

/note="L2 repeat: matches 1754. .2097 of consensus"

24291. .24581

/note="Alusx repeat: matches 1. .300 of consensus"

24653. .24850

/note="MAR repeat: matches 1. .200 of consensus"

26189. .26685
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82767. .32830
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19642. 19716

//note="MIR repeat: matches 48. 131 of consensus"

19969. 20010

//note="21 copies 2 mer tg 100% conserved"

20623. 20704
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33050. .33178
                                                                                                                   100.25. .10/US
//note="MIR repeat: matches 60. .140 of consensus"
16928. .16993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .138 of consensus"
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35551, 35604
/note="27 copies 2 mer ac 94% conserved"
37585, 38254
                                                                                                                                                                                       conserved"
                                   oţ
                                109
                                                                                                                                                                                                                                                                                                                                                              19169. 19400
Noote- MIR repeat: matches 5. 239
10456. 19627
Noote-"LIMC5 repeat: matches 7728.
                                   repeat: matches 9.
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                                                                           /note="MIR repeat: matches 3.
16626. .16705
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note="MIR repeat: matches
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/note="CpG 1sland"
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Direct Submission
Submitted (12-JUL-2001) Sanger Centre, Hinxton, Cambridgeshire,
CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone
requests: clonerequest@sanger.ac.uk
On Jul 8, 2001 this sequence version replaced gi:14575291
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequences with
This sequence was finished as follows unless otherwise noted: all
                                                                                                                                                                                                                                                                                                                                                                                                                                            assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMEL; WORNPEP; Information on the WORNPEP database can be found at
                                                                                                                                                                                                                                                                                  This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >- 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mapping Group. Further information can be found at http://www.sanger.ac.uk/HGP/Chrl0
RPI1-34331 is from the library RPCI-11.2 constructed by the group of Pieter de Jong. For further details see http://www.chori.org/Dacpac/home.htm
VECTOR: pBACG3.6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 10, constructed by the Sanger Centre Chromosome 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This sequence is the entire insert of clone RPI1-343J3 The true left end of clone RPI1-242G20 is at 139955 in this sequence. The true right end of clone RPI1-404C6 is at 6588 in this sequence. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6916. 8080
/note="LIMEc repeat: matches 1168. .2367 of consensus"
9934. .10087
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5662, .6438
/note="LIMEc repeat: matches 272, .1095 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4319. 4494
/note="mluSx repeat: matches 118. .293 of consensus"
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4577. .14633
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2. .142 of consensus"
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note="AluSg repeat: matches 1. .310 of consensus"
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14372. .14576
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .194 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          151. .293
/note="MIR repeat: matches 2. .148 of consensus"
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12479. .12608
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/note-"MIR repeat: matches 65.
11077. .11372
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/note="AluSx repeat: matches
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/db_xref="taxon:9606"
/chromosome="10"
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/clone_lib="RPCI-11.2"
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Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Anderson, S., Baldwin, J., Barna, N., Beckerly, R., Beda, F., Boguslavkly, L., Boukhagalter, B., Brown, A., Burkett, G., Castle, A., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P.,
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Birren, B., Linton, L., Nusbaum, C. and Lander, E.
Homo sapiens chromosome 10, clone RP11-57E12
                                                                                                                                                                                                                                                                                                   /4153. 1443/9
//note="THEIC repeat: matches 1. 371 of consensus"
//note="LTRI6A repeat: matches 90. 445 of consensus"
/5046--LTRI6A repeat: matches 37. 97 of consensus"
/5240. 45300
//note="LTRA1 repeat: matches 90. 192 of consensus"
//note="LTRA1 repeat: matches 90. 192 of consensus"
/6826. 46871
//note="23 copies 2 mer gt 97% conserved"
50684. 50969
//note="Aluga repeat: matches 1. 287 of consensus"
50980. 51291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          54261. :54432
/note="FAM repeat: matches 2. .167 of consensus"
54433. :54629
/note="LIM4 repeat: matches 3652. .3865 of consensus"
54648. :54842
/note="LIR41 repeat: matches 11. .217 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             note-"L1M4 repeat: matches 3865. .4055 of consensus"
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/note="LTR41 repeat: matches 217. .716 of consensus"
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/note="MiT1Al repeat: matches 1. .365 of consensus"
55237. .55700
                                                                                                                                    #1296. 41460

#1296. 41460

#1296. 41460

#1296. 2730 of consensus"

#1506. 41944

#1506. 2730 of consensus"

#1506. 41944

#1506. 2416 of consensus"

#15388. 42698

#44193. 44579
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                 /note-"MIR repeat: matches 1. .144 of consensus"
41057. .41290
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Pred. No. 8.6e-07;
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HTG; HTGS_PHASE1; HTGS_DRAFT.
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Best Local Similarity 100.0
Matches 32; Conservative
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DeArellano, K., Dewar, K., Domino, M., Doyle, M., Fenestor, J., FitzHugh, W., Forrest, C., Gage, D., Galagan, J., Gardyna, S., Grant, G., Hagos, B., Haeford, A., Horton, L., Howland, J.C., Johnson, R., Hacker, K., Kann, L., Karatas, A., Klein, J., Landers, T., Lehoczky, J., Levine, R., Lieu, C., Liu, G., Locke, K., Marquis, M., McEwan, P., McGurk, A., McKernan, K., McPheeters, R., Meldrim, J., Meneus, L., Morrow, J., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P., Olivar, T.M., Peterson, K., Pierre, N., Pisanl, C., Pollara, V., Raymond, C., Riley, R., Rothman, D., Stojanovic, N., Subramanian, N., Talamas, J., Tesfaye, S., Theodore, J., Tirrell, A., Vassiliev, H., Viel, R., Vo, A., Wu, X., Hyman, D., Ye, W.J., Direct, S., Lander, A. and Zody, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Direct Submitsed Carbon Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA Research, 320 Charles Street, Cambridge, MA 02141, USA CENTERS STREET, Cambridge, MA 02141, USA CENTERS STREET, Nusbaum, C., Lander, E., Abraham, H., Allen, N., Anderson, S., Baldwill, J., Barna, N., Bastien, V., Beda, F., Boukhgalter, B., Brown, A., Burkett, G., Campopiano, A., Cooke, P., DeArellano, K., Dewar, G., Collins, S., Golde, S., Golde, S., Goyette, M., Graham, L., Karatas, A., Klein, J., Laronno, M., Doyle, M., Ferreira, P., Fitzhugh, W., Gage, D., Grand-Plerre, N., Grant, G., Lilev, I., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., Larongoue, K., Landers, T., Lehoczky, J., Levine, R., Lieu, C., Liu, G., Locke, K., Macdonald, P., Marquis, N., McEwan, P., McGurk, A., McKernan, K., McPheeters, R., Leu, G., Liu, G., Lui, G., Lui, G., Murphy, T., Naylor, J., Mihova, T., Miranda, C., Mlenga, V., Morrow, J., Murphy, T., Naylor, J., Norman, C. H., O'Connor, T., O'Connor, T., O'Connel, P., Pleani, C., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Trigillo, J., Voassiller, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W. Submitted Calamer, A. and Zody, M. Trigillo, J., Voassiller, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, Wo, Submitted Calamer, A. and Zody, M. Trigiller, E. Submitted Calamer, Van Research, 320 Charles Street, Cambridge, MA 02141, USA
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Center: Whitehead Institute/ MIT Center for Genome Research
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Insert size: 171041; sum-of-contigs
Quality coverage: 3.7 in Q20 bases; agarose-fp
Quality coverage: 3.8 in Q20 bases; sum-of-contigs
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Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
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Center clone name: 57_E.12

Sequencing vector: M13; M73815, 100% of reads chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.960731

Consensus quality: 161190 bases at least Q30

Consensus quality: 166837 bases at least Q30

Consensus quality: 166895 bases at least Q20
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Web site: http://www.seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Direct Submission
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06499 106598: gap of 100 bp 116986: contlg of 10388 bp in length 116987 117086: gap of 100 bp 100 bp 118990: gap of 100 bp 100 bp 118990: gap of 100 bp 100 bp 1187391 147290: contig of 13300 bp in length 47391 173341: contig of 25951 bp in length.
                                                                                                          3144 5889; contig of 2746 bp in length 5890 5989; app of 100 bp 8779; contig of 2990 bp in length 8980 9079; gap of 100 bp 100 b
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Best Local Similarity 100.0%; Pred. No. 8.6e-07;
Matches 32; Conservative 0; Mismatches 0;
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Human Neurogenin-3 PCR primer used to

Mouse neurogenin 1 Murine neurogeninDNA encoding human Human NeuroD2 gene Human reproductive Human reproductive Human immune/haema

Oligonucleotide fo Acetylcholine tran nAChR beta2 subuni M. capsulatus gene

Oligonucleotide fo Human immune/haema

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capsulatus capsulatus

Human reproductive

Human immune/haema

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Basic helix-loop-helix; BHLH; RELAX; Rat Embryonic Longitudinal Axis; control; gene expression; transcriptional activator; targeting; protein expression; central nervous system; CNS; treatment; nervous system disorder; ss.
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              GenCore version 5.1.4\_p5\_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                                                         The present sequence encodes a basic helix-loop-helix (BHLH) type protein, designated RELAX (Rat Embryonic Longitudinal Axis) protein. The protein is used to control and participate in gene expression, by acting as transcriptional activator, strictly dependent on the presence of an intact E box (CANNTG), particularly for targeting expression of proteins to the central nervous system (CNS). The nucleic acid sequence can be used to treat nervous system disorders, and antisense sequences can be used to control mRNA transcription.
                                                                                                                                                                                                                                                                                                                  1 GCAGGTAGCGAGGAGCAGTCCCTGGGCCCCCGTTGCTGATTGCCCCGTGGCACAGGCA
                                                                                                                                                                                                                                                                                                                                                          121 CGATTAGCAGCTCAGAAGTCCCTCTGGGTCTCACCACTGCACAGAGGCCGAGGACCCCT
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                                                Basic helix-loop-helix polypeptide and related nucleic acid
transcriptional activity, for targeting expression of genes
central nervous system and treatment of nervous disease
                                                                                                                                                                                                                                              0; Indels
                                                                                                                                                                                                     Sequence 1491 BP; 307 A; 487 C; 413 G; 284 T; 0 other;
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                                                                                                                                                                                                                        100.0%; Score 1460;
100.0%; Pred. No. 0;
tive 0; Mismatches
Icard-Liepkalns
                                                                                       Claim 6; Page 20; 28pp; French
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Ravassard
                   WPI; 1998-362775/31
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                       CCAACGACCGGGAGCGCAACCGCATGCACATAACTTCAACTCCGCGCTGGATGCGCTGCGCG
                                                                                      GTGTCCTGCCCACCTTCCCGGATGACGCCAAACTTACAAAGATCGAGACCCTGCGCTTTCG
                                                                                                             CCCACAACTACATTTGGGCACTGACTCAGACGCTGCGCATAGCGGACCACAGCTTCTACG
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/product= "Mouse neurogenin 3"
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The patent discloses a method for inducing non-neuronal cells (NNC) to differentiate into neurons and for NNCs to express a neuronal subtype specific marker. Transformed host cells are used as sources of neuronal and other growth factors; in culture for screening compounds that modulate neural differentiation or as sources of recombinantly produced methodate neural differentiation cas sources of recombinantly produced to neuropanis and Phox2a proteins for use in transplantation. The cells also have a variety of in vivo uses, e.g. for transplantation at sites of neuronal dystunction e.g. patients with hearing or vision loss due to optical or auditory nerve damage, brain or spinal cord injuries, and neurodespenerative disorders e.g. Alzheimer's disease. The present sequence encodes murine neurogenin 3 (NGN 3), a transcription factor that induces a core program of neurogenesis. Forced expression of murine NGN3 can elicit expression of at least some neuronal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Atonal; homologue; orthologue; atonal-associated protein; deafness; hearing impairment; vestibular effect; balance disorder; osteoarthritis; cellular proliferation; cerebellar granule neuron; gene therapy; mechanoreceptive cell growth; auditory; osteopathic; cytostatic;
                                                                                                                                                                                                                     Inducing non-neuronal cells to differentiate into neurons and for non-neuronal cells to express a neuronal subtype-specific marker, comprising contacting the non-neuronal cells with a vector containing neurogenin nucleic acid -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            762 GCGCTGGATGCGCTGCGCGGTGTCCTGCCCACCTTCCCGGATGACGCCAAACTTACAAAG 821
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 804 BP; 171 A; 263 C; 225 G; 145 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mouse neurogenin 3 (ngn3) cDNA, SEQ ID NO:24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6.3%; Score 92; DB 100.0%; Pred. No. 9.3 iive 0; Mismatches
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                                                                                    (CALY ) CALIFORNIA INST OF TECHNOLOGY.
                                                                                                                                                                                                                                                                                                                                             Claim 1; Fig 1J; 76pp; English.
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nes 92, Conservative
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                                                                                                                                                                                            P-PSDB; AAY70570
                                                                                                                            Anderson DJ,
13-AUG-1999;
                                          14-AUG-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        neurogenin 3 is one of several neurogenin proteins discussed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            in the present invention. The neurogenin nucleic acids can be express in a host cell, transformed using an expression vector, to produce recombinant proteins. The proteins and the antibodies raised against the proteins are useful in the study of neurogenesis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     neurogenins, useful in neurogenesis - and recombinant nucleic and proteins derived from rat and Xenopus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 804;
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/product= "Murine neurogenin-3 protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 804 BP; 171 A; 263 C; 225 G; 145 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ouery Match 6.3%; Score 92; DB 19; L
Best Local Similarity 100.0%; Pred. No. 9.3e-35;
Matches 92; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Murine neurogenin-3 (NGN3) nucleic acid sequence.
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                                                                                                        97WO-US17048
                                                                                                                                                97US-0932411
                                                                                                                                                                  96US-0722570.
                                                                                                                                                                                                              96US-0772009
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                                                                                                                                                                                                                                                                                              Anderson DJ, Ma O,
                                                                                                                                                                                                                                                                                                                                               WPI; 1998-230702/20.
                                                                                                                                                                                                                                                                                                                                                                     P-PSDB; AAW54947
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                                                                                                          24-SEP-1997;
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                                                                02-APR-1998
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                                                                                                                                                                        17-SEP-1996
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DB 21; Length 804; 9.3e-35;

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The invention relates to the use of atonal-associated nucleic acid or amino acid sequence, or any of its homologues or orthologues as therapeutic agents for the treatment of deafness, partial hearing loss, vestibular effects due to damage or loss of inner hair cells, osteoarthritis and abnormal cell proliferation. The invention also encompasses methods of screening for compounds which affect the expression of an atonal-associated nucleic acid sequence in an animal, cand a transgenic animal in which an allele of a native atonal-associated and a transgenic animal in which an allele of a native atonal-associated in activating the atonal-associated allele. The nucleic acids or proteins inactivating the atonal-associated allele. The nucleic acids or proteins may be used in a method of treating an animal for hearing impairment, of joint disease, balance disorders, abnormal cell proliferation, or other classes related to loss of a functional aconal-associated nucleic acid or protein. The may may particularly be used to treat an animal with a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               also be used in promoting mechanoreceptive cell growth and generating hair cells. The present sequence represents an atonal-associated nucleic acid sequence referred to in the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 or their precursors, and may
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  463 GCGCTGGATGCGCTGCGCGGTGTCCTGCCCACCTTCCCGGATGACGCCAAACTTACAAAG 522
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                                                                                                                                                                                                   Therapeutic use of atonal-associated nucleic acids or amino acids, or any of its homologs or orthologs, for the treatment of e.g. deafness, osteoarthritis and abnormal cell proliferation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          the present sequence is not shown in the specification, but
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                                                                                                    Ben-Arie N;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6.3%; Score 92; DB 22; Length 861;
100.0%; Pred. No. 9.3e-35;
Live 0; Mismatches 0; Indels
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                                                                                                    Hassan B,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          protein, They may particularly be used to deficiency in cerebellar granule neurons
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1093.1737
/*tag= a
/product= "Ngn3"
/note= "Neurogenin 3"
                                                                                                    Birmingham N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                   Disclosure; Page -; 142pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAC61090 standard; DNA; 1861 BP
                                                          (BAYU ) BAYLOR COLLEGE MEDICINE
          19-JAN-2000; 2000US-0176993.
  990S-0137060
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  05-FEB-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    was obtained from GenBank
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     92; Conservative
                                                                                                  Bellen H,
                                                                                                                                          WPI; 2001-032190/04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
                                                                                                                                                             P-PSDB; AAB60359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus
01-JUN-1999;
                                                                                                  Zoghbi HY,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAC61090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Note:
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Gaps

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The human neurogenin 3 Ngn3 DNA sequence AAC61089 encodes the Ngn3 protein AAY85617. The Ngn3 gene is located at chromosome position 10q22.1-22. The invention relates to the human Ngn3 nucleotide and 10q22.1-22. The invention relates to the human Ngn3 nucleotide and protein sequences, and includes an antibody recognising the Ngn3 protein. Also included in the invention is a method for identifying an islet cell precursor. The method involves analysing a cell for the expression of the Ngn3 gene product, where detection of the product is indicative of an islet cell precursor. The Ngn3 DNA sequence is useful as a diagnostic reagent for detecting (in a subject) a predisposition to a defect in Ngn3 activity. The Ngn3 protein is useful for identifying beta-cell precursor cells expressing Ngn3, and to alter cellular differentiation in outline in vivo to produce new beta-cells to treat patients with diabetes mellitus. The present sequence represents the murine Ngn3 genomic DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Atonal; homologue; orthologue; atonal-associated protein; deafness; hearing impairment; vestibular effect; balance disorder; osteoarthritis; cellular proliferation; cerebellar granule neuron; gene therapy; mechanoreceptive cell growth; auditory; osteopathic; cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1396 GCGCTGGATGCGCTGCGCGGTGTCCTCCCCGGATGACGCCAAACTTACAAAG 1455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    762 GCGCTGGATGCGCTGCGCGGGTGTCCTGCCCACCTTCCGGGATGACGCCAAACTTACAAAG 821
                                                                                                                                                                                                                                                                                             Novel human neurogenin 3 polypeptides and polynucleotides encoding them, useful for diagnosis, prevention and treatment of diabetes mellitus and to identify individuals at risk of diabetes -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6.3%; Score 92; DB 21; Length 1861;
100.0%; Pred. No. 9e-35;
ive 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mouse atonal homologue 5 (ATOH5, Math4B) cDNA, SEQ ID NO:4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1861 BP; 397 A; 560 C; 537 G; 367 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1456 ATCGAGACCCTGCGCTTCGCCCACACTACAT 1487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               853
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                                                                                                                                                                                                                                                                                                                                                                             Claim 18; Page 49-50; 54pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAF27254 standard; cDNA; 5567 BP
                                                                             28-MAR-2000; 2000WO-US08436.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
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                                                                                                                                                         (REGC ) UNIV CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            transgenic animal; ss
                                                                                                                                                                                                                                      WPI; 2000-664989/64.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity
                                                                                                                                                                                                 German MS, Lin J;
                                                                                                                                                                                                                                                          P-PSDB; AAY85618.
WO200059936-A1.
                                                                                                                      06-APR-1999;
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                                          12-OCT-2000
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WO200073764-A2.

07-DEC-2000.

S & Carry)

Mus musculus.

Faigler S;

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The present invention describes oligonucleotide libraries for detecting messenger RNAs that populate a (sub.)transcriptome where the (sub.)transcription comprises messenger RNAs transcribed from multiple transcription units that populate a genome. The library comprises c transcription units that populate a genome. The library comprises several oligonucleotides, each capable of hybridising selectively to a several oligonucleotide libraries are useful for detecting mult of the oligonucleotide libraries are useful for detecting mRNAs from a complex in expression profiling studies, in qualitatively or detecting RNA transcripts and splice variants of human or animal cranscriptomes. The libraries may also be used as specialised mind libraries to detect transcripts of a sub-transcriptome under a particular biological or pathology-specific genes such as those genes conly expressed in specific tissue under a specific pathological conly expressed in specific tissue under a specific pathological condition; to detect developmental specific genes such as those genes conly expressed in specific under a specific pathological condition; to detect developmental specific genes such as those genes condition; to detect developmental specific genes such as those genes conjugated and splice variants of a transcriptome of a patient suffering from a patricular disorder. ABNA7253 to ABNA7589 represent conficient of the printed of the present invention. Or the exemplification of the present invention form part of the printed specification of the present invention or such as obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                           New oligonucleotide libraries comprising oligonucleotides which selectively hybridize to mRNAs transcribed from a transcription unit of a genome, useful for detecting tissue-, pathology-, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1252 TTCCTTGCTGCTGTGCGTGCACAAGGACATTGCAGGCTGATCTCCTCTTAACCCTCCTC 1311
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 65 BP; 11 A; 20 C; 14 G; 20 T; 0 other;
                                                                                                                                                                                                          Mintz E, Mintz L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 1; SEQ ID 4140; 47pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                              developmental-specific genes
                                                                        28-JUL-2000; 2000US-221607P.
02-MAY-2001; 2001US-287724P.
                      20-JUL-2001; 2001WO-IB01903
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                                                                                                                                                                                                          Wasserman
                                                                                                                                                     (COMP-) COMPUGEN INC
                                                                                                                                                                                                                                                            WPI; 2002-257383/30.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABN57521;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     anino acid sequence, or any of its homologues or orthologues as the interpretatic agents for the treatment of deafness, partial hearing loss, vestibular effects due to damage or loss of inner hair cells, osteoarthritis and abnormal cell proliferation. The invention also encompasses methods of screening for compounds which affect the capression of an atonal-associated nucleic caid sequence in an animal, and a transgenic animal in which an allele of a native atonal-associated allele. The nucleic acids or proteins may be used in a method of treating an animal for hearing impairment, joint disease, balance disorders, abnormal cell proliferation, or other of assase related to loss of a functional aconal-associated nucleic acids or protein. They may particularly be used to treat an animal with a deficiency in cerebellar granule neurons or their precursors, and may also be used in promotting mechanoreceptive cell growth and generating that cells. The present sequence represents an atonal-associated nucleic acid or acid sequence referred to los the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               762 GCGCTGGATGCGCTGCGCGGTGTCCTGCCCACCTTCCCGGATGACGCCAAACTTACAAAG 821
                                                                                                                                                                                                                                                                                                                                       Therapeutic use of atomal-associated nucleic acids or amino acids, or any of its homologs or orthologs, for the treatment of e.g. deafness, osteoarthritis and abnormal cell proliferation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to the use of atonal-associated nucleic acid or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Note: The present sequence is not shown in the specification, but was obtained from GenBank.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rat spliced transcript detection oligonucleotide SEQ ID NO:4140.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 5567;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 349 C; ....; Score 92; DB 22; Lengum -: "red. No. 8.5e-35; Indels
                                                                                                                                                                                                          Ben-Arie N;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 5567 BP; 1271 A; 1549 C; 1564 G; 1183 T; 0 other;
                                                                                                                                                                                                             B,
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100.0%; Pred. No. e...
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                                                                                                                                                                                                          Birmingham N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Page -; 142pp; English.
                                                                                                                                                  (BAYU ) BAYLOR COLLEGE MEDICINE
           01-JUN-2000; 2000WO-US15410.
                                                                        01-JUN-1999; 99US-0137060.
19-JAN-2000; 2000US-0176993.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        92; Conservative
                                                                                                                                                                                                          Zoghbi HY, Bellen H,
                                                                                                                                                                                                                                                            WPI; 2001-032190/04.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
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Matches

ð g ò RESULT 7 **ABN31392**

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Gaps

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Mouse spliced transcript detection oligonucleotide SEQ ID NO:30269. Human; mouse; rat; splice transcript; detection; RNA transcript; splice variant; transcriptome; oligonucleotide library; ss.

Mus musculus

Rattus norvegicus

WO200210449-A2

Shoshan A,

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Novel human neurogenin 3 polypeptides and polynucleotides encoding them, useful for diagnosis, prevention and treatment of diabetes mellitus and to identify individuals at risk of diabetes
                                                                                                           /note= "Neurogenin 3"
                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 6; Page 46-48; 54pp; English.
                                                                  /*tag= a
/product= "Ngn3"
                                                                                                                                                                                                                                                28-MAR-2000; 2000WO-US08436.
                                      3022..3666
/*tag= a
                                                                                                                                                                                                                                                                                                                                           (REGC ) UNIV CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2000-664989/64.
P-PSDB; AAY85617.
                                                                                                                                                                                                                                                                                                                                                                                        German MS, Lin J;
                                                                                                                                                        WO200059936-A1
                                                                                                                                                                                                                                                                                           06-APR-1999;
                                                                                                                                                                                                     12-OCT-2000
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                     Key
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The oligonucleotide libraries are useful for detecting manage from a biological sample, in expression profiling studies, in qualitatively characterising the corresponding transcriptome, and in qualitatively characterising the corresponding transcriptome, and in factoring RNA transcripts and splice variants of human or animal transcriptomes. The libraries may also be used as specialised minimaries to detect transcripts of a sub-transcriptome under a particular biological or pathology specific genes such as those genes only expressed in specific tissue under a specific pathological conjugation of tissue- and pathology specific genes; and to detect RNA transcripts and splice variants of a transcriptome of a patient suffering from a particular disorder. ABN27253 to ABN59589 represent coligonucleotide sequences from rate, humans and mice, which are used in the exemplification of the present invention.

N.B. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp. wipo.int/pub/published_pot_sequences.
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                                                                                                                                                                                                                                                                                                                                                            New oligonucleotide libraries comprising oligonucleotides which selectively hybridize to mRNAs transcribed from a transcription unit of a genome, useful for detecting tissue-, pathology-, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              present invention describes oligonucleotide libraries for detecting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              transcription units that populate a genome. The library comprises several oligonucleotides, each capable of hybridising selectively to a set of messenger RNAs transcribed from a given transcription unit of the genome, which encodes one or more messenger RNA splice variants.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      messenger RNAs that populate a (sub-)transcriptome, where the (sub-)transcriptome comprises messenger RNAs transcribed from multiple
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Neurogenin 3; Ngn3; chromosome 10q22.1-22.2; cellular differentiation; islet cell precursor identification; diabetes mellitus; human; ds.
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                                                                                                                                                                                                                                                                        Faigler S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 65 BP; 16 A; 25 C; 11 G; 13 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human neurogenin 3 (Ngn3) genomic DNA sequence.
                                                                                                                                                                                                                                                                        Mintz E, Mintz L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2.4%; scc. 100.0%; Pred. No. c. 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 547 TCAGTTCCAATTCCACCCACCTAGCCCCACTCTC 581
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 TCAGTTCCAATTCCACCCACCTAGCCCCACTCTC 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 1; SEQ ID 30269; 47pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAC61089 standard; DNA; 5340 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                 developmental-specific genes
                                                                                                        20-JUL-2001; 2001WO-IB01903.
                                                                                                                                                      28-JUL-2000; 2000US-221607P. 02-MAY-2001; 2001US-287724P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     05-FEB-2001 (first entry)
                                                                                                                                                                                                                                                                      Wasserman A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    35; Conservative
                                                                                                                                                                                                                           (COMP-) COMPUGEN INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity
                                                                                                                                                                                                                                                                                                                 WPI; 2002-257383/30.
                   WO200210449-A2.
                                                              07-FEB-2002
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The human neurogenin 3 Ngn3 DNA sequence AAC61089 encodes the Ngn3 protein AAY85617. The Ngn3 gene is located at chromosome position protein aavenue.

10422.1-212. The invention relates to the human Ngn3 nucleotide and protein sequences, and includes an antibody recognising the Ngn3 protein. Also included in the invention is a method for identifying an islet cell precursor, the method involves analysing a cell for the expression of the Ngn3 gene product, where detection of the product is indicative of an islet cell precursor. The Ngn3 DNA sequence is useful as a diagnostic reagent for detecting (in a subject) a predisposition to a defect in pancreatic islet cell function or formation associated with a defect in practicity. The Ngn3 protein is useful for identifying beta-cell precursor cells expressing Ngn3, and to alter cellular differentiation in culture in vivo to produce new beta-cells to treat patients with diabetes
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; foetal tissue antigen; ss; antiinflammatory; neuroprotective;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      immunomodulator; cardiovascular; cytostatic; nephrothropic; cardiovascular; autoimmune disease; rheumatoid arthritis; hyperproliferative disorder; breast neoplasm; cancer; cardiovascular disorder; cardiac arrest; cerebrovascular disorder; cardiac arrest; cerebral ischaemia; angiogenesis; nervous system disorder; Alzheimer's disease; infection; ocular disorder; corneal infection; wound healing; epithelial cell proliferation; food additive.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 5340;
                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 5340 BP; 1215 A; 1500 C; 1514 G; 1111 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human cDNA encoding a novel foetal antigen, SEQ ID No 321.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 21; L
2.1e-05;
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3235 AAGAGCGAGTTGGCACTGAGCAAGCAGCGACG 3266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         672 AAGAGCGAGTTGGCACTGAGCAAGCAGCGACG 703
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 32;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2.2%; s
100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAS33797 standard; cDNA; 428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 100.0
....hes 32; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17-DEC-2001 (first entry)
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Query Match

Matches

ö q Homo sapiens.

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(HUMA-) HUMAN GENOME SCI INC
                                                                                                  17-JAN-2001; 2001WO-US01321
                                WO200155312-A2
Homo sapiens
                                                                  02-AUG-2001
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WPI; 2002-537346/57

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The invention relates to novel nucleic acids encoding novel human foetal antigens. The nucleic acids and proteins are used to prevent, treat (e.g. antigens. The nucleic acids and proteins are used to prevent, treat (e.g. rabbits, goats, horses, cats, dogs, chickens or sheep. They care also used in diagnosing a pathological condition or susceptibility to a pathological condition. The antibodies to the antigens can also conclude the alleviating symptoms associated with the disorders and in diagnostic immunosasays e.g. radioimmunoassays or enzyme linked immunosorbent assays (ELISA). Disorders which are diagnosed or treated immunosorbent assays (ELISA). Disorders which are diagnosed or treated conclude autoimmune diseases e.g. rheumatoid arthritis, cardiovascular disorders e.g. radial arrest, cerebrovascular disorders e.g. cardiac aused by bacteria, viruses and fungion sold out a disorders e.g. corneal intection asystem disorders e.g. corneal interview by preptices can also be used to ald wound healing and epithelial cell proliferation, to responsibilities, fat content, ilpid, protein, candorders e.g. crapablities, fat content, lipid, protein, candorders e.g. capablities, fat content, lipid, protein, cambohydrate, virusins, capanierals, cofactors and disorders treated by the nucleic acids and examples of diseases and disorders treated by the nucleic acids and proteins are given in the specification. The present sequence
                                                                                                                      preventing or prognosing e.g. diseases or disorders of the nervous, musculoskeletal, excretory, gastrointestinal, reproductive, and respiratory systems
                                                                                                                                                                                                                                                                          Claim 1; SEQ ID No 321; 642pp; English
                     Ruben SM;
                       Barash SC,
                                                                         WPI; 2001-488782/53.
                                                                                               P-PSDB; AAU20977
                       Rosen CA,
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Gaps ô Score 29; DB 22; Length 428; Pred. No. 0.0007; 0; Indels 100.0%; Pred. M. + + ve 0; Mismatches . 60. Local Similary, Query Match Matches

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825 GAGACCCTGCGCTTCGCCCACACTACAT 853 1 GAGACCCTGCGCTTCGCCCACAACTACAT 29 õ g

Human Neurogenin-3 gene PCR primer SEQ ID NO: 221. ABT03700 standard; DNA; 26 BP 13-SEP-2002 (first entry) ABT03700; RESULT 11 ABT03700/

Human; cancer; neoplastic disease; tumour specific marker; cytostatic; transcription factor; PCR; primer;

Homo sapiens.

WO200240716-A2

23-MAY-2002.

13-NOV-2001; 2001WO-US43461

16-NOV-2000; 2000US-249508P

(CEMI-) CEMINES LLC

Palm K;

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The present invention relates to a method for determining the presence of neoplastic molecular markers in a host, involving the use of neoplastic molecular marker specific reagents to detect such markers and analysing the array of reagents, allowing the identification of the neoplastic disease present. This can be used to determine the best treatment for cancers, in particular neural cell, lung and prostate tumours. The present sequence is a pCR primer useful for detecting the coding sequences of markers of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PCR primers AAV42515-16 are used to isolate part of the DNA encoding a basic helix-loop-helix (BHLH) type protein, designated RELAX (Rat Embryonic Longitudinal Axis) protein. The PCR product is termed CIG235. The protein is used to control and participate in gene expression, by acting as transcriptional activator, strictly dependent on the
                                                                      Determining the presence of neoplastic molecular markers, by identifying the presence of markers in host test sample using array of neoplastic molecular marker specific reagents and analyzing the array
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Basic helix-loop-helix; BHLH; RELAX; Rat Embryonic Longitudinal Axis; control; gene expression; transcriptional activator; targeting; protein expression; central nervous system; CNS; treatment; nervous system disorder; CIG235; PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             - with
to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PCR primer used to isolate part of the RELAX protein coding region.
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transcriptional activity, for targeting expression of genes
central nervous system and treatment of nervous disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1.8%; Score 26; DB 24; Length 26; 100.0%; Pred. No. 0.024; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Seguence 26 BP; 3 A; 10 C; 5 G; 8 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 673 AGAGCGAGTTGGCACTGAGCAAGCAG 698
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26 AGAGCGAGTTGGCACTGAGCAAGCAG 1
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                                                                                                                                                                                                                                                      Example 1; Page 17; 41pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (RHON ) RHONE-POULENC RORER SA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 100.0
Matches 26; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1998-362775/31.
                                                                                                                                                                                             the reagents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19-DEC-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rattus sp.
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Gaps

us-09-595-947c-1.rng

304 GAGCGCAACCGCATGCACAACCT 326

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Anderson DJ,
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                                                                                                                                                                        04-JUL-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24-FEB-2000
                                                                                                                                    AAZ51977;
                                                                                                                                                                                                                                                                                                                                                                                            Mus sp.
                                                                           AAZ51977
                                                           RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           the present invention. The neurogenin nucleic acids can be expressed in a host cell, transformed using an expression vector, to produce recombinant proteins. The proteins and the antibodies raised against the proteins are useful in the study of neurogenesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The mouse neurogenin 1 is one of several neurogenin proteins discussed
                                                                                                                                                                            Gaps
presence of an intact E box (CANNTG), particularly for targeting expression of proteins to the central nervous system (CNS). The nucleic acid sequence came be used to treat nervous system disorders, and antisense sequences can be used to control mRNA transcription.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             neurogenins, useful in neurogenesis - and recombinant nucleic and proteins derived from rat and Xenopus
                                                                                                                                                                          ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; neurogenin; expression vector; recombinant protein; neurogenesis.
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                                                                                                                                      Length 25;
                                                                                                                                                                            Indels
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                                                                                               C; 6 G; C
1.7%; Score 25; DB 19; Le
7. Pred. No. 0.073;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /*tag= a
/product= "Mouse neurogenin 1"
                                                                                               Sequence 25 BP; 5 A; 9 C; 6 G; 5 T; 0 other;
                                                                                                                                                    Local Similarity 100.0%; Pred. No. 0.000 Pred. No. 0.0000 Pred. No. 0.0000 Pred. 0.0000 Pred. Nismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                 750 AACCITAACICCGCGCIGGAIGCGC 774
                                                                                                                                                                                                                                     1 AACCTTAACTCCGCGCTGGATGCGC 25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sommer L;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           97US-0932411.
96US-0722570.
96US-0030864.
96US-0772009.
                                                                                                                                                                                                                                                                                                                                                     AAV27046 standard; cDNA; 738
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                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mouse neurogenin 1 gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17-SEP-1997;
27-SEP-1996;
12-NOV-1996;
19-DEC-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    02-APR-1998
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antibody; n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
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                                                                                                                                        Query Match
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The patent discloses a method for inducing non-neuronal cells (NNC) to differentiate into neurons and for NNCs to express a neuronal subtype specific marker. Transformed host cells are used as sources of neuronal and other growth factors; in culture for screening compounds that modulate neural differentiation or as sources of recombinantly produced neuroganins and phox2a proteins for use in transplantation. The cells also have a variety of in vivo uses, e.g. for transplantation at sites of neuronal dysfunction e.g. patients with hearing or vision loss due to optical or auditory nerve damage, brain or spinal cord injuries, and neurodegenerative disorders e.g. Alzheimer's disease. The present sequence encodes murine neuroganin-1 (NGN-1), a transcription factor. NNCS differentiate into neurons through the recombinant expression of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
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                                                                                                                                                                                                                                                                                      Neurogenin-1; NGN-1; non-neuronal cell; NNC; neurogenesis; Phox2a protein; neuronal subtype-specific marker; growth factor; neurolal differentiation; transplantation; neuronal dysfunction; optical nerve damage; auditory nerve damage, neurodegenerative disorder; neuroprotective; nootropic; anticonvulsant; antiParkinsonlan; vulnerary; cerebroprotective; immunesuppressant; antilnfectious; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    non-neuronal cells to differentiate into neurons and for non-neuronal cells to express a neuronal subtype-specific marker, comprising contacting the non-neuronal cells with a vector containing neurogenin nucleic acid .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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100.0%; Pred. No. 0.59;
1ve 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product= "Murine neurogenin-1 protein"
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                                                                                                                                                                                                                       (NGN1) nucleic acid sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
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   BP.
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AA251977 standard; DNA; 738
                                                                                                                                                    (first entry)
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P-PSDB; AAY70566.
                                                                                                                                                                                                                               Murine neurogenin-1
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732 GAGCGCAACCGCATGCACAACCT 754

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Gaps

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732 GAGCGCAACCGCATGCACAACCT 754

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Conservative

Local Similarity nes 23; Conserv

Best Loc Matches

Search completed: April 8, 2003, 21:20:26 Job time : 404 secs

304 GAGCGCAACCGCATGCACAACCT 326

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amino acid sequence, or any of its homologues or orthologues as therapeutic agents for the treatment of deafness, partial hearing loss, vestibular effects due to damage or loss of inner hair cells, osteoarthritis and abnormal cell proliferation. The invention also encompasses methods of screening for compounds which affect the expression of an atomal-associated nucleic acid sequence in an animal, and a transgenic animal in which an allele of a native atomal-associated gene is replaced by a heterologues nucleic acid sequence, thus inactivating the atomal-associated allele. The nucleic acids or proteins may be used in a method of treating an animal for hearing impairment, joint disease, balance disorders, abnormal cell proliferation, or other disease related to loss of a functional atomal-associated or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        protein. They may particularly be used to treat an animal with a deficiency in cerebellar granule neurons or their precursors, and may also be used in promoting mechanoreceptive cell growth and generating hair cells. The present sequence represents an atomal-associated nucleic acid sequence referred to in the invention.
                                                                                                                                                                                                    Atonal; homologue; orthologue; atonal-associated protein; deafness; hearing impairment; vestibular effect; balance disorder; osteoarthritis; cellular proliferation; cereblar granule neuron; gene therapy; mechanoreceptive cell growth; auditory; osteopathic; cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to the use of atonal-associated nucleic acid or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Therapeutic use of atonal-associated nucleic acids or amino acids, or any of its homologs or orthologs, for the treatment of e.g. deafness, osteoarthritis and abnormal cell proliferation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Note: The present sequence is not shown in the specification, but was obtained from GenBank.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ben-Arie N;
                                                                                                                                                              Chicken atonal homologue ngn2/ath4a cDNA, SEQ ID NO:20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 790 BP; 91 A; 351 C; 283 G; 65 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hassan B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Zoghbi HY, Bellen H, Birmingham N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Page -; 142pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (BAYU ) BAYLOR COLLEGE MEDICINE.
                                        AAF27264 standard; cDNA; 790 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-JUN-2000; 2000WO-US15410.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-JUN-1999; 99US-0137060
19-JAN-2000; 2000US-0176993.
                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                  transgenic animal; ss
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                                                                                AAF27264;
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Gaps

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1.6%; Score 23; DB 22; Length 790; Best Local Similarity 100.0%; Pred. No. 0.59; Matches 23; Conservative

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(without alignments)
7808.933 Million cell updates/sec
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                                                                                                                    April 8, 2003, 21:09:53; Search time 164 Seconds
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GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                        593429 seqs, 438583890 residues
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Post-processing: Listing first 45 summaries
                                                                                  OM nucleic - nucleic search, using sw model
                                                                                                                                                                                                                                                                                           OLIGO_NUC
Gapop 60.0 , Gapext 60.0
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Maximum DB seq length: 200000000
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1460
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Perfect score:
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                                                                                                                       Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

/cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*/cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq:*/cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*/cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*/cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

// Cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
// cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
// cgn2_6/ptodata/2/pubpna/US06_BYEW_PUB.seq:*
// cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
// cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
// cgn2_6/ptodata/2/pubpna/US08_BYEW_PUB.seq:*
// cgn2_6/ptodata/2/pubpna/US08_BYEW_PUB.seq:*
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// cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
// cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*

					SUMMARIES	
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Result		Query				
No.	Score	Match	Match Length DB	DB	QI	Description
	92	6.3	645		US-10-004-717-4	Sequence 4, Appli
7	92	6.3	861	σ	US-10-004-717-24	Sequence 24, Appl
m	92	6.3	1861	10	US-09-817-360-3	Sequence 3, Appli
4	32	2.2	5340	10	US-09-817-360-1	Sequence 1, Appli
ľ	23	1.6	738	7	US-08-722-570-13	Sequence 13, Appl
9	23	1.6	790	σ	US-10-004-717-20	Sequence 20, Appl
7	23	1.6	1385	σ	US-10-004-717-30	~
80	23	1.6	1412	6	US-10-004-717-6	Sequence 6, Appl1
σ	23	1.6	1412	6	US-10-004-717-37	Sequence 37, Appl
c 10	20	1.4	352	10	US-09-728-445-108	Sequence 108, App
c 11	19	1.3	200	10	US-09-783-590-2157	Sequence 2157, Ap
c 12	19	1.3	1263	σ	US-09-938-842A-1036	Sequence 1036, Ap
13	18	1.2	4797	10	US-09-751-797-25	Sequence 25, Appl
c 14	18	1.2	20272	10	US-09-908-711-145	Sequence 145, App
c 15	18	1.2	25619	10	US-09-908-711-143	Sequence 143, App
c 16	18	1.2	25619	10	US-09-764-898-302	Sequence 302, App
c 17	18	1.2	31728	σ	US-10-114-170-64	Sequence 64, Appl
18	18	1.2	402850	σ	US-09-844-653-5	Sequence 5, Appli
19	17	1.2	31	10	US-09-817-360-17	Sequence 17, Appl

Sequence 14228, A Sequence 6887, Ap Sequence 1714, Ap Sequence 1094, Ap Sequence 257, App Sequence 257, App Sequence 21148, A Sequence 313, App Sequence 313, App Sequence 7938, App Sequence 7938, App Sequence 75, App Sequence 75, App Sequence 75, App Sequence 208, App Sequence 2159,	Sequence 137, App
10 US-09-960-352-14228 10 US-09-960-352-6887 10 US-09-960-352-6887 10 US-09-960-352-6887 10 US-09-783-590-12149 10 US-09-864-761-257 10 US-09-864-761-334 10 US-09-864-761-334 10 US-09-864-761-334 10 US-09-864-761-332 10 US-09-864-761-332 10 US-09-864-761-332 10 US-09-864-761-332 10 US-09-864-761-332 10 US-09-910-498 10 US-09-815-242-438 10 US-09-815-242-858 10 US-09-815-242-858 10 US-09-815-242-858	US-09-764-868-137
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ALIGNMENTS

RESULT 1 O - 00 C - 10 - 00 C - 0 C - 0 C C C C C C C C C C C	RESULT 1 Sequence 4, Application US/10004717 Sequence 4, Application US/10004717 Publication No. US20020192665A1 GENERAL INFORMATION: APPLICANT: ZOGHBI, HUDA Y. APPLICANT: ZOGHBI, HUDA Y. APPLICANT: ZOGHBI, HUDA Y. TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPEUTIC USE OF AN TITLE OF INVENTION: APONAL ASSOCIATED SEQUENCE FOR DEAFNESS, TITLE OF INVENTION: OSTEDARTHRITIS, AND ABNORMAL CELL PROLIFERATION TITLE OF INVENTION: OSTEDARTHRITIS, AND ABNORMAL CELL PROLIFERATION TITLE OF INVENTION: OSTEDARTHRITIS, AND ABNORMAL CELL PROLIFERATION CURRENT PELING DATE: 2002-08-16 PRIOR PELING DATE: 2000-01-19 PRIOR PELING DATE: 2000-01-19 PRIOR PELING DATE: 1099-06-01 NUMBER OF SEQ ID NOS: 69 SOFTWARE: PATENTIN Ver. 2.1 SEQ ID NO 4 LENGTH: 645 TYPE: DNA TYPE: DNA NUMBER: MUS MUSCULUS COGNANISM: MUS MUSCULUS	
Ouery Best Match	Ouery Match 6.3%; Score 92; DB 9; Length 645; Best Local Similarity 100.0%; Pred. No. 5.5e-39; Matches 92; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
Qy 7 Db 3	762 GCGCTGGATGCGCTGCGCGGTGTCCTGCCCGGATGACGCCAAACTTACAAAG 821 	
Qy 8	822 ATCGAGACCCTGCGCTTCGCCCACAACTACAT 853	

RESULT 2 US-10-004-717-24 g

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Sequence 1, Application US/09817360

Patent No. US20020015696A1

GENERAL INFORMATION:
APPLICANT: German, Michael S.
APPLICANT: Lin, Joseph
TITLE OF INVENTION: PRODUCTION OF PANCREATIC ISLET CELLS
FILE REFERENCE: UCSF-129CIP
CURRENT FILING DATE: 2001-03-20
PRIOR PELICATION NUMBER: 09/535,145
PRIOR PELICATION NUMBER: 60/128,180
PRIOR PELING DATE: 1999-04-06
NUMBER OF SEQ ID NOS: 19
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1
LENGTH: 5340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: United States

ZIP: 94111-4187

COMPUTER READALE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/722,570
FILING DATE: 27-SEP-1996
CLASSIFICATION NUMBER: 38.55
ATTORNEY/AGENT INFORMATION:
NAME: S11va, RODIN M.
REGISTRATION NUMBER: 38.304
REGISTRATION NUMBER: A +6.3902/RFT/RMS
TELECOMMUNICATION: INFORMATION:
TELECOMMUNICATION INFORMATION:
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Publication No. US20030044887A1
GENERAL INFORMATION:
APPLICANT: Anderson, David J.
APPLICANT: Ma, Qilfu
TITLE OF INVENTION: NEUROGENIN
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: Flehr, Hobbach, Test, All
STREET: Four Embarcadero Center, Su
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (415) 398-3249
0 277299
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LENGTH: 738 base pairs
TYPE: nucleic acid
STRANDEDNESS: unknown
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
CORGANISM: Homo Sapiens
US-09-817-360-1
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US-08-722-570-13
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                                                                              APPLICANT: ZOGHBI, HUDA Y.

APPLICANT: ZOGHBI, HUDA Y.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPEUTIC USE OF AN TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPEUTIC USE OF AN TITLE OF INVENTION: OSTEOARTHRITIS, AND ABNORMAL CELL PROLIFERATION FILE REPERRORE: 105/10/004,717

CURRENT APPLICATION NUMBER: US/10/004,717

CURRENT PILING DATE: 2000-01-09

PRIOR PELLING DATE: 2000-01-19

PRIOR APPLICATION NUMBER: 60/17,060

PRIOR APPLICATION NUMBER: 60/137,060

PRIOR APPLICATION NUMBER: 60/137,060

PRIOR FILING DATE: 1999-06-01

NUMBER OF SEQ ID NOS: 69

SOFTWARE: PALENTH VET. 2.1

SEQ ID NO 24
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Best Local Similarity 100.0%; Pred. No. 5e-39;
Matches 92; Conservative 0; Mismatches 0; Indels
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Patent No. US20020015696A1
GENERAL INFORMATION
GENERAL INFORMATION
GENERAL APPLICANT: GENERAL, Michael S.
APPLICANT: Lin, Joseph
TITLE OF INVENTION: PRODUCTION OF PANCREATIC ISLET CELLS
TITLE OF INVENTION: AND DELIVERY OF INSULIN
FILE REFERENCE: UCSF-129CIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ouery Match 6.3%; Score 92; DB 9; Le
Best Local Similarity 100.0%; Pred. No. 5.4e-39;
Matches 92; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/817,360
CURRENT FILING DATE: 2001-03-20
PRIOR APPLICATION NUMBER: 09/535,145
PRIOR FILING DATE: 2000-03-24
PRIOR APPLICATION NUMBER: 60,128,180
PRIOR FILING DATE: 1999-04-06
NUMBER OF SEQ ID NOS: 19
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 3
LENGTH: 1861
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   822 ATCGAGACCCTGCGCTTCGCCCACAACTACAT 853
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      523 ATCGAGACCCTGCGCTTCGCCCACACTACAT 554
Sequence 24, Application US/10004717 Publication No. US20020192665A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; ORGANISM: Mus musculus US-10-004-717-24
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US-09-817-360-3
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US-09-817-360-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
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Gaps

Indels

Length 5340;

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Sequence 6, Application US/10004717

Publication No. US2002019265A1

| GENERAL INFORMATION:
| APPLICANT: ZOGHBI, HUDA Y. |
| APPLICANT: YANG, OI
| TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPEUTIC USE OF AN ITILE OF INVENTION: OSTEOARTHRITIS, AND ABNORMAL CELL PROLIFERATION |
| TITLE OF INVENTION: OSTEOARTHRITIS, AND ABNORMAL CELL PROLIFERATION |
| TITLE OF INVENTION: OSTEOARTHRITIS, AND ABNORMAL CELL PROLIFERATION |
| TITLE OF INVENTION: OSTEOARTHRITIS, AND ABNORMAL CELL PROLIFERATION |
| FILE REPRENCE: 1004004, 717 |
| CURRENT FILING DATE: 2000-06-01 |
| PRIOR FILING DATE: 2000-06-01 |
| PRIOR FILING DATE: 2000-01-19 |
| PRIOR FILING DATE: 1999-06-01 |
| PRIOR APPLICATION NUMBER: 60/137,060 |
| PRIOR FILING DATE: 1999-06-01 |
| NUMBER: OF SEQ ID NOS: 699
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APPLICANT: ZOGHBI, HUDA Y.

APPLICANT: ZOGHBI, HUDA Y.

APPLICANT: TANG, OI

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPEUTIC USE OF AN TITLE OF INVENTION: ATONAL ASSOCIATED SEQUENCE FOR DEAFNESS, TITLE OF INVENTION: OSTEOARFHRITIS, AND ABNORMAL CELL PROLIFERATION CURRENT APPLICATION NUMBER: US/10/004,717

CURRENT APPLICATION NUMBER: 09/585,645

PRIOR APPLICATION NUMBER: 60/176,993

PRIOR APPLICATION NUMBER: 60/176,993

PRIOR APPLICATION NUMBER: 60/176,993

PRIOR FILING DATE: Z000-01-19

PRIOR FILING DATE: 1999-06-01
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                                                          Score 23; DB 9; Length 138:
Pred. No. 0.036;
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Pred. No. 0.036;
0; Mismatches (
                                                                1.6%; Scor.
100.0%; Pred. No. v.
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; Sequence 37, Application US/10004717
; Publication No. US20020192665A1
; GENERAL INFORMATION:
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Best Local Similarity 100.0%; P
Matches 23; Conservative 0;
                                                                                 Query Match 1.67
Best Local Similarity 100.(
Matches 23; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Ver. SEQ ID NO 6 LENGTH: 1412
  ; ORGANISM: Mus musculus
US-10-004-717-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; ORGANISM: Mus musculus US-10-004-717-6
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SEQ ID NO 37
LENGTH: 1412
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Sequence 30, Application US/2002192665A1

GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: ZOGHBI/*HUDA Y.

APPLICANT: ZOGHBI/*HUDA Y.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPEUTIC USE OF AN TITLE OF INVENTION: ATONAL ASSOCIATED SEQUENCE FOR DEAFNESS,

TITLE OF INVENTION: COMPOSITIONS AND ABNORMAL CELL PROLIFERATION

FILE REFERENCE: P01899US4

CURRENT FILING DATE: 2002-08-16

PRIOR FILING DATE: 2000-06-01

PRIOR PAPLICATION NUMBER: 60/176,993

PRIOR FILING DATE: 2000-01-19

PRIOR FILING DATE: 1999-06-01

NUMBER OF SEQ ID NOS: 69

SEGTRARE PATENTING DATE: 1999-06-01

NUMBER OF SEQ ID NOS: 69
                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION NO. 19200192665A1

Sequence 20, Application US/10004717

PUBLICANT: 20GHBI, HUDA Y.

APPLICANT: ZOGHBI, HUDA Y.

APPLICANT: YANG, QI

TITLE OF INVENTION: ACONPOSITIONS AND METHODS FOR THE THERAPEUTIC USE OF AN TITLE OF INVENTION: ACONPOSITIONS AND ABNORWAL CELL PROLIFERATION TITLE OF INVENTION: ACONTAINS ASSOCIATED SEQUENCE FOR DEAFWESS,

TITLE OF INVENTION: ACONTAINS AND ABNORWAL CELL PROLIFERATION FILE REFERENCE: P01899US4

CURRENT APPLICANTION NUMBER: 09/10/004,717

CURRENT FILING DATE: 2000-06-01

PRIOR FILING DATE: 2000-06-01

PRIOR FILING DATE: 2000-06-01

PRIOR PELING DATE: 2000-06-01

PRIOR PELING DATE: 2000-06-01

PRIOR PILING DATE: 1999-06-01

NUMBER OF SEQ ID NOS: 69

SEQ ID NO 20

MANDER OF SEQ ID NOS: 69

LENGTH: 790

MANDER OF SEQ ID NOS: 69

LENGTH: 700

MANDER OF SEQ ID NOS: 69
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                                                                                                       Query Match 1.6%; Score 23; DB 7; Length 738; Best Local Similarity 100.0%; Pred. No. 0.038; Matches 23; Conservative 0; Mismatches 0; Indels
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Best Local Similarity 100.0%; Pred. No. 0.038;
Matches 23; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                   304 GAGCGCAACCGCATGCACAACCT 326
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  unknown
; TOPOLOGY: unknowr; MOLECULE TYPE: DNA US-08-722-570-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TYPE: DNA
; ORGANISM: chicken
US-10-004-717-20
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LENGIH: 1385
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RESULT 12
US-09-938-842A-1036/c
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APPLICANT: Zambrowicz, Brian
APPLICANT: Sands, Arthur T.
TITLE OF INVENTION: No. US20020102543Alel Mutated Mammalian Cells and
TITLE OF INVENTION: Animals
FILE REFERENCE: LEX-0102-USA
CURRENT PAPLICATION NUMBER: US/09/728,445
CURRENT FILING DATE: 2000-11-30
PRIOR FILING DATE: 1999-12-01
NUMBER OF SEQ ID NOS: 891
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 108
LENGTH: 352
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APPLICANT: Haseltine, William A.
APPLICANT: Li, Hacodong
APPLICANT: Li, Hacodong
APPLICANT: Scen, Craig A.
APPLICANT: Ruben, Steven M.
TITLE OF INVENTION: Human Genes, Sequences, and Expression Products 16.2
FILE REFERENCE: PO-416.2C1
CURRENT APPLICATION NUMBER: 08/420,856
PRIOR PLICATION DATE: 1995-04-12
PRIOR PLICATION DATE: 1995-04-12
PRIOR PLICATION DATE: 1995-04-12
PRIOR PLICATION DATE: 1995-04-12
PRIOR PLILING DATE: 1994-11-21
                                                                                 Gaps
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                                       Score 23; DB 9; Length 1412;
Pred. No. 0.036;
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1.6;
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                                                                                 Mismatches
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OTHER INFORMATION: n equals a,t,g, or NAME/KEY: misc feature
LOCATION: (207)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2157, Application US/09783590 Patent No. US20020110850A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                             Sequence 108, Application US/09728445 Patent No. US20020102543A1
                                            100.0%; Pre
                                                                                                                                          445 GAGGGCAACCGCATGCACAACCT 467
                                                                                                                     732 GAGCGCAACCGCATGCACAACCT 754
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Best Local Similarity 100.0%; P
Matches 20; Conservative 0;
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APPLICANT: Friedrich, Glenn
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                                     Query Match 176
Best Local Similarity 100.
Matches 23; Conservative
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; ORGANISM: Mus musculus
US-09-728-445-108
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ORGANISM: Homo sapiens
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US-09-783-590-2157/c
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LENGTH: 500
US-10-004-717-37
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GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Kreps, Joel

APPLICANT: Wang, Xun

APPLICANT: Wang, Xun

APPLICANT: Tan, Tong

TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINI:

TITLE OF INVENTION: SAME, AND METHODS OF USE

FILE REFERENCE: SCRIP1300-3

CURRENT APPLICATION NUMBER: US/09/938,842A

CURRENT FILING DATE: 2001-08-24
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5.4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
CAGATION: (441)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
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) OTHER INFORMATION: n equals a,t,g, or c
US-09-783-590-2157
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PRIOR APPLICATION NUMBER: US 60/227,866
PRIOR FILING DATE: 2000-08-24
PRIOR APPLICATION NUMBER: US 60/264,647
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/300,111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LOCATION: (379)
OTHER INFORMATION: n equals a,t,g, or
NAME/KEY: misc feature
                                                                                                                                                                                                            OTHER INFORMATION: n equals a,t,g, or NAME/KEY: misc feature
                                                                                                                                                                                                                                                                                or
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  or
                                    LOCATION: (215)
OTHER INFORMATION: n equals a,t,g, or NAME/KEY: misc feature
LOCATION: (324)
OTHER INFORMATION: n equals a,t,g, or NAME/KEY: misc feature
                                                                                                                                                                                                                                                                                                                                                                                           LOCATION: (369)
OTHER INFORMATION: n equals a,t,g,
NAME/KEY: misc feature
WATION: n equals a,t,g,
lsc feature
                                                                                                                                                                                                                                                        LOCATION: (360)
OTHER INFORMATION: n equals a,t,g,
NAME/KEY: misc feature
                                                                                                                                                                                                                                                                                                                         LOCATION: (368)
OTHER INFORMATION: n equals a,t,g,
NAME/KEY: misc feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1319 CCACCTCAAACTCCCGCTC 1337
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Length 20272;
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PRIOR PELICATION NOMBER: 0501/01349
PRIOR APPLICATION NUMBER: 09/764,902
PRIOR PELICATION NUMBER: 09/764,902
PRIOR PELICATION NUMBER: 0501/0139
PRIOR PELICATION NUMBER: 09/764,870
PRIOR PELICATION NUMBER: 09/764,870
PRIOR PELICATION NUMBER: 0501/01348
PRIOR FILING DATE: 2001-01-17
PRIOR PELICATION NUMBER: 05/764,882
PRIOR FILING DATE: 2001-01-17
PRIOR FILING DATE: 2001-01-17
PRIOR FILING DATE: 2001-01-17
PRIOR PELICATION NUMBER: 05/764,882
PRIOR FILING DATE: 2001-01-17
PRIOR APPLICATION NUMBER: 09/764,896
PRIOR FILING DATE: 2001-01-17
PRIOR APPLICATION NUMBER: 09/764,896
PRIOR FILING DATE: 2001-01-17
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PRIOR FILING DATE: 2000-06-07
NUMBER OF SEQ ID NOS: 167
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 145
LENGTH: 20272
                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: 09/764,898
APPLICATION NUMBER: 09/764,898
                                                                                                                                                                                                   FILING DATE: 2001-01-17
APPLICATION UNMBER: 09/764,869
FILING DATE: 2001-01-17
APPLICATION NUMBER: US01/01340
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PRIOR APPLICATION NUMBER: 09/764,853
PRIOR FILING DATE: 2001-01-17
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PRIOR APPLICATION NUMBER: US01/01349
                                                                                                         FILING DATE: 2001-01-17
APPLICATION NUMBER: 09/764,891
FILING DATE: 2001-01-17
APPLICATION NUMBER: US01/01339
                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: 09/764,874 FILING DATE: 2001-01-17 APPLICATION NUMBER: US01/01334
                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: US01/01320
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                                                                                                                                                                                                                                                                                                   ING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Dumoutter, Laure
APPLICANT: Louned, Jamila
APPLICANT: Renauld, Jaen-Christophe
TITLE OF INVENTION: (TIFs) The Proteins Encoded, and Uses Thereof
TITLE OF INVENTION: (TIFs) The Proteins Encoded, and Uses Thereof
TITLE OF INVENTION: (TIFs) The Proteins Encoded, and Uses Thereof
CURRENT APPLICATION NUMBER: US/09/751,797
CURRENT FILING DATE: 1999-10-18
PRIOR FILING DATE: 1999-10-18
PRIOR FILING DATE: 1999-10-26
NUMBER OF SEQ ID NOS: 29
SEQ ID NO 25
LENGTH: 4797
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CURRENT APPLICATION NUMBER: US/09/908,711
CURRENT FILING DATE: 2001-07-20
PRIOR APPLICATION NUMBER: US/1/01360
PRIOR FILING DATE: 2001-01-17
PRIOR APPLICATION NUMBER: US01/01345
PRIOR FILING DATE: 2001-01-17
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 25, Application US/09751797
Patent No. US20010024652A1
GENERAL INFORMATION:
                                                                                          TYPE: DNA ORGANISM: Arabidopsis thaliana
                                                                                                                                                                                                                                                                             658 GGCGCAACAGGCCCAAGAG 6,76
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                                                                                                                                                                                                                                                                                                   599 GGCGCAACAGGCCCAAGAG 581
PRIOR FILING DATE: 2001-06-22
NUMBER OF SEQ ID NOS: 5379
SEQ ID NO 1036
LENGTH: 1263
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Best Local Similarity 100.
Matches 18; Conservative
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US-09-908-711-145/c
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US-09-751-797-25
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Search completed: April 8, 2003, 23:20:39
Job time : 285 secs
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CURRENT APPLICATION NUMBER: US/01-01-7

PRIOR FILING DATE: 2001-01-7

PRIOR PELING DATE: 2001-01-7

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PRIOR FILING DATE: 20.010-11.
PRIOR FILING DATE: 2001-01-17
PRIOR FILING DATE: 2001-01-17
PRIOR FILING DATE: 2001-01-17
PRIOR FILING DATE: 2001-01-17
PRIOR APPLICATION NUMBER: US01/01347
PRIOR FILING DATE: 2001-01-17

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PRIOR APPLICATION NUMBER: US01/01347
PRIOR FILING DATE: 2001-01-17
PRIOR APPLICATION NUMBER: 09/764,896
PRIOR FILING DATE: 2001-01-17
PRIOR APPLICATION NUMBER: US01/01307
PRIOR FILING DATE: 2001-01-17
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US-09-908-711-143/c
Sequence 143, Application US/09908711
; Patent No. US20020045230A1
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6642 TCAGAGCTGTCTGAAATG 6625
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Pred. No. 13;
0; Mismatches 0
                                    PRIOR FILING DATE: 2001-01-17
PRIOR APPLICATION NUMBER: 09/764,868
PRIOR FILING DATE: 2001-01-17
PRIOR FILING DATE: 2001-01-17
PRIOR FILING DATE: 2001-01-17
PRIOR FILING DATE: 2000-01-31
PRIOR FILING DATE: 2000-01-31
PRIOR APPLICATION NUMBER: 60/180,628
PRIOR FILING DATE: 2000-02-04
PRIOR FILING DATE: 2000-06-07
PRIOR FILING DATE: 2000-06-07
PRIOR FILING DATE: 2000-06-07
SOFTWARE: PALENTIN NOMBER: 60/209,467
PRIOR FILING DATE: 2000-06-07
SOFTWARE: PALENTIN VER: 2.0
SEQ ID NO 143
LENGTH....
FILING DATE: 2001-01-17
APPLICATION NUMBER: US01/01336
FILING DATE: 2001-01-17
APPLICATION NUMBER: 09/764,868
FILING DATE: 2001-01-17
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100.0%; Pre
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Best Local Similarity 100.0
Matches 18; Conservative
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; ORGANISM: Homo saptens
US-09-908-711-143
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Gaps

1048 TCAGAGCTGTCTGAAATG 1031

Title: Perfect score:

Sequence:

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Scoring table:

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B1445873 dai33504.
AV944801 AV944801
BM255695 514849 MA
AV939670 AV939670
AL173398 TERTRACHON
BM810917 AGENCOURT
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AV286451 RPCT-23-1
BF191558 29141 MA
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AZ985482 ZM0267B19
AU057600 AU057600
BM030263 488856 MA
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BM088009 501361 MA
AQ594075 HS_5334_A
AM67224 LG1_358_C
AV597322 AV597322
AQ631359 RPCI-11-4
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                    AZ506899 1M0348GI3
BE263765 601194122
B1910102 603067946
BF204175 601867625
AU067624 AU067624
BQ686909 AGENCOURT
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Eukaryota, hetazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 593)
Eahao, S., Niezman, W., Feldblyum, T., Malek, J., Shatsman, S., Akinret.
1, B., Levins, M., Mcgann, S., Tsegaye, G., Geer, K., Krol, M., de Jong, P.
and Fraser, C.M.
                                                                                         BM563662 AGENCOURT
BE780690 601469349
BG419220 602445870
                                                                                                                            AA113743 W5F Pyroc
T70947 yc49c05.rl
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Clones are derived from the mouse BAC library RPCI-23. For BAC
library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mouse BAC End Sequences from Library RPCI-23 Unpublished (1999)
Other GSSs: RRCI-23-160G18.TJ
Contact: Shaying 12a0
Department of Eukaryotic Genomics
The Institute for Genomic Research 7712 Medical Center Dr., Rockville, MD 20850, USA 7712 Medical Center Dr., Rockville, MD 20850, USA Fax: 301 838 0200
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BE936551
AQ753599
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BB071548
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BG808248 2083-52 M
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BG854922 1024041C0
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                                                                                 April 8, 2003, 20:42:04; Search time 2260 Seconds (without alignments) 10462.571 Million cell updates/sec
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            GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                       TITLE
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                                                                                                                                                                                                                                                                                                                                                    /note="Organ: Kidney/Brain; Vector: pBACe3.6; Site_1:
brain genomic DNA was isolated and partially digested
with a combination of EcoRI and EcoRI Methylase. Size
selected DNA was cloned into the pBACe3.6 vector at the
ECORI sites. The ligation products were transformed into
DH10B electrocompetent cells (BRL Life Technologies).
159 c 1313 g 133 t
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MUS MUSCULUS AGULT MALE SMALL INTESTINE CDNA, RIKEN full-length
enriched library, clone:201001M19:atonal homolog 5 (Drosophila),
full insert sequence.
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BACPAC Resources (http://bacpac.med.buffalo.edu/orderingframe.htm) or from Resea ch Genetics (info@resgen.com). BAC end page: http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html plate:ifo row: G column: 18 Seq primer: T7 Class: BAC ends.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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                                                                                                                                                                                        /organism-"Mus musculus"
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                                                                                                                                                                                                                                                                                                                              /lab_host="DH10B"
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Kawai, J., Shinaqawa, A., Shibata, K., Yoshino, M., Itoh, M., Ishii, Y., Arakawa, T., Hara, A., Fukunishi, Y., Konno, H., Adachi, J., Fukuda, S., Alaswa, T., Imara, A., Fukunishi, Y., Konno, H., Adachi, J., Fukuda, S., Alaswa, M., Ishii, K., Ishono, H., Kasukawa, T., Santo, R., Kadota, K., Matsuda, H., Ashburner, M., Batalov, S., Casavant, T., Rachann, W., Gasterland, T., Gissi, C., King, B., Kochiwa, H., Kuchi, P., Lewis, S., Matsuo, Y., Nikaido, I., Pesole, G., Yochiwa, H., Kuchi, P., Lewis, S., Matsuo, Y., Nikaido, I., Pesole, G., Washio, T., Sakai, K., Okido, T., Furuno, M., Aono, H., Baldarelli, R., Barsh, G., Blake, J., Boffelli, D., Bojunga, N., Carninci, P., Ge Bonaido, M. F., Brownstein, M. J., Bult, C., Fletcher, C., Fujita, M., Gariboldi, M., Gustincich, S., Hill, D., Marchionni, L., Mashima, J., Mazzarelli, J., Mombaerts, P., Nordone, P., Ring, B., Ringwald, M., Rodriguez, I., Sakamoto, N., Sasaki, H., Toyo-oka, K., Wang, K.H., Weitz, C., Whittaker, C., Wilming, L., Wynshaw-Boris, A., Yoshida, K., Hasegawa, Y., Kawaji, H., Kottsuki, S., and Hayashizaki, Y., Yoshida, K., Hasegawa, Y., Kawaji, H., Kottsuki, S., and Hayashizaki, Y.
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Adachi, J., Aizawa, K., Akahira, S., Akimura, T., Aono, H., Arai, A., Arakawa, T., Baldarelli, R., Bono, H., Brownstein, M., Bult, C., Carninci, P., Fukuda, S., Fukunishi, Y., Furuno, M., Hanagaki, T., Hara, A., Hayatsu, N., Hill, D., Hiramoto, K., Haraka, T., Horli, F., Hume, D., Imotani, K., Ishii, Y., Itoh, M., Izawa, M., Kasukawa, T., Kato, H., Kavai, J., Kojima, Y., Koudo, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazati, A., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Okazaki, Y., Okido, T., Owa, C., Quackenbush, J. Saito, H., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D., Schrimi, L., Shibata, X., Shibata, Y., Shibata, Y., Shibata, Y., Shibata, Y., Shibata, Y., Tayami, M., Tagawa, A., Takahashi, F., Yasunishi, A., Yoshida, K., Yoshino, M., Muramatsu, M., and Hayashizaki, Y. Somission

Li Submitted (10-010-2000) Yoshihide Hayashizaki, The Institute of Chiman Chillian, M., Chana, M., Chana
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Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y. RIKBN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer Genome Res. 10 (11), 1757-1771 (2000)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Functional annotation of a full-length mouse cDNA collection Nature 409 (6821), 685-690 (2001)
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/organism="Mus musculus"

source

Gaps

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01 M-EVO-bwt-k-07-0-UI.Il NIH BMAP_EVO Mus musculus cDNA clone
IMAGE:5701758 5', mRNA sequence.
BQ178789
BQ178789.1 GI:20354281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       pcMVSPORT 6 vector. Library was constructed by Life Technologies. Contact: Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville Maryland 20850, USA Fax: (1) 301 610 8371 Email:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note-"Organ: Fetal brain; Vector: pCMVSFORT 6; 1st strand
CADA was primed with a NotL-oilgo(dT) primer. Five prime
end enriched, double-stranded cDNA was digested with Not I
and cloned into the Not I and Eco RV sites of the
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information regarding entire library may be found at http://pga.swmed.edu/Data/Libraries/microarray_cdna_libraries.htm."
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Li, W.B., Gruber, C., Jessee, J. and Polayes, D. Full-length cDNA libraries and normalization Unpublished (2001)
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BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
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                                                                                                                               /tissue_type="small intestine"
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/dev_stage="adult"
1. 1540
                                                                                                                                                                                                                                                                                                                                                                                    /procein_id="Bab25411.1"
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PGGGSNGDWGSIXSYVSQAGNLSPTASLEEFPGLQVPSSPSYLLPGALVFSDFL"
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2083-52 Mouse E14.5 retina lambda ZAP II Library Mus musculus cDNA,
mRNA sequence.
BG808248
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 600)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone_lib="Mouse E14.5 retina lambda ZAP II Library"
/tissue_type="neural retina"
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                                                                                                                                                                                                                                                                                            /note="atonal homolog 5 (Drosophila)
data source:MGD, source key:MGI:893591, evidence:ISS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Department of Blochemistry and Molecular Biology University of Texas M.D. Anderson Cancer Center Box 117, 1515 Holcombe Blvd., Houston, TX 77030, USA Fax: 713 790 0329.
      /strain_"C57BL/6J"
/db_xref="FANTOM_DB:2010001M19"
/db_xref="MGD:MGI:1907403"
/db_xref="taxon:10090"
/db_ore="2010001M19"
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                                                                                                                                                                                                                                                                                                                                                                    /codon_start=1
                                                                                                                                                                                                                         /gene="Atoh5"
241. .885
                                                                                                                                                                                                                                                       241. .885
/gene="Atoh5"
                                                                                                                     /sex="male"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1. .600
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Gaps

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Analyses of the Chlamydomonas reinhardtii Genome: A Model,
Unicellular System for Analyzing Gene Function and Regulation in
             Vascular Plants: project phase 2 Unpublished (2000)
Contact: Charles Hauser
DONB Box 91000
                                                                                                                                                                                                                    /organism-"Chlamydomonas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Smail: asimpson@ludwig.org.br
                                                                                                                                                                   Email: chauser@duke.edu.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1244 CGGAGGCGCAACAGGCCCAAGA 1266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          653 CGGAGGCGCAACAGGCCCAAGA 675
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Simpson A.J.G
                                                                                                     Duke University
Durham, NC 27708-1000
Tel: 919 613 8159
Fax: 919 613 8177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tel: +55-11-2704922
Fax: +55-11-2707001
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Best Local Similarity 100..
Pest Local 3; Conservative
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                                                                                                                               Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs.r@mail.nih.gov
Tissue Procurement: Dr. James Lin, Univeristy of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: MGC clone distribution information can be
ffound through the I.M.A.G.E. Consortium/LLNL at:
This clone was contributed by the Brain Molecular Anatomy Project
(BMAP)
                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. I tosas: 1 to 814)
NHF-MGC http://mgc.ncl.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chlamydomonas reinhardtii.
Chlamydomonas reinhardtii
Eukaryota, Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
Chlamydomonadaceae; Chlamydomonas.
1 (bases 1 to 1269)
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1024041C06.y2 C. reinhardtil CC-1690, normalized, Lambda 2ap II
Chlamydomonas reinhardtil cDNA, mRNA sequence.
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McDermott,J.P., Silflow,C., Stern,D. and Surzycki,R.
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100.0%; Pred. No. 1.6;
Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                   /organism-"Mus musculus"
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                   house mouse
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BG854922
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/note="Vector: pBluescript II SK-; Site_I: ECORI; Site_2:
Xhoi; This library, constructed by John Davies and Jeffrey
McDermott, combines cDNAs from CC-1690 cells grown to
mid-log phase in TAP (actate-containing) medium in the
light, TAP medium in the dark, HS (minimal) medium in the
light, TAP medium in the dark, HS (minimal) medium in
ambient levels of CO2 and HS medium bubbled with 5% CO2.
PolyA mRNA was purified from each sample, pooled and cDNA
synthesized. The cDNA was directionally cloned into lambda
ZAP II (Stratagene) in the EcoRI (5') and XhoI (3') sites,
pBluescript II SK- plasmids were excised from the lambda
ZAP clones by superinfection with Exassist (Stratagene)
phage. The library was normalized using method 4 described
in Bonaldo et al (1996) Genome Research 6: 791-806."
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                                                                                                                                                                    'clone_11b="C. reinhardti1 CC-1690, normalized, Lambda Zap
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1 (bases 1 to 319)
1 blases 1 to 119)
1 blas Neto.E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carraho,A.F., Matsukuma,A., Bais,G.S., Simpson,D.H.,
Brunstein,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
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/strain="CC-1690 wild type mt+ 21gr" /db_xref="taxon:3055"
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1.7;
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100.0%; Pred. No. 1...
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101
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                                                                                                                                                              106 CAAGIGICCCAAGAGACCCAG 126
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                                                                                                                                           492 CAAGTGTCCCAAGAGACCCAG
  O
  114
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                                                                                                                                                                                                                                                                                                                                                                                                                   house mouse.
                                                                               Best Local Similarity
Matches 21; Conserv
  125 a
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 464)
Mahairas, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T.,
Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D. and
                                                                                                                                                              /organism="Homo sapiens"
/db_xref="taxon:9606"
/db_xref="taxon:9606"
/dc.cone_lib="NT0053"
/dc.ga="Adult"
/note="Organ: nervous_tumor; Vector: puc18; Site_1: SmaI;
Site_2: SmaI; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwfg.org.br/scripts/gethtml2.pl?tl=&t2=RC5-NT0053-310 800-024-5016x13-2000-08-31&t4-1)
Seq primer: puc 18 forward Seq primer: puc 18 forward High quality sequence stop: 319.
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464 bp DNA linear GSS 22-JUL-199
HS_2117_A2_H03_MR CIT Approved Human Genomic Sperm Library D Homo
saplens genomic clone Plate=2117 Col=6 Row=0, DNA sequence.
AQ753599.1 GI:5578650
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Clones may be purchased from Research Genetics (info@resgen.com).
BAC end Web Server: http://www.htsc.washington.edu
Plate: 2117 row: 0 column: 6
Seq primer: M13 Reverse
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/db_xref="taxon:9606"
/clone="Plate=2117 Col=6 Row=0"
/clone_lib="CIT Approved Human Genomic Sperm Library D"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome
Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
99380589
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            High Throughput Sequencing Center University of Washington 401 Queef Anne Avenue North, Seattle, WA 98109, USA Tel: (206) 616-3887 Emx: (206) 616-3887 Email: jwallace@u.washington.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 319;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 12;
15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Mahairas GG, Wallace JC, Hood L
                                                                                                                                                                                                                                                                                                                                                                        low stringency conditions."
87 c 106 g 73 t
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 21;
Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ouery Match
Best Local Similarity 100.0
Matches 21, Conservative
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ORIGIN
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AUTHORS
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KEYWORDS
SOURCE
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AQ753599
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Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Weiss Blomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
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                                                                                                                                                                                                                                                                                                                                                                                                                              AZ506899 536 bp DNA linear GSS 05-OCT-2000 IM0348G13F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0348G13 F, DNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Cranlata; Vertebrata; Euteleostom!;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

[ (bases 1 to 536)
Dunn, D., Aoyadi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly,
M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.
and Wright, D., Weiss, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /lab_host_"E. Coll strain XLIO-Gold, T1-resistant, F-"/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mouse whole genome scaffolding with paired end reads from 10kb
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/strain="c57BL/6J"
/db_xref="taxon:10090"
/clone="UGCIMO348613"
/clone_lib="Mouse 10kb plasmid UUGCIM library"
                                                                                                                                                     ..
                                                                                            Length 464;
                                                                                                                                                        Indels
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                                                                                            17;
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Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0348 row: G column: 13
Seq primer: CGTTGTAAAACGACGCCGCAGT
Class: plasmid ends
                                                                                      core 21; DB 1
red. No. 16;
Mismatches
123
                                                                                            Score 21;
Pred. No.
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   Б
                                                                                         1.4%; Scc
llarity 100.0%; Pi
Conservative 0;
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ORIGIN

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BF204175 913 bp mRNA linear EST 06-NOV-2000 601867625F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4110222 5',
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National Institutes of Health, Mammalian Gene Collection (MGC)
Lonpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATC
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Preparation: Ling Hong/Rubin Consortium (LINL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: LLCM996 row: a column: 07
High quality sequence stop: 714.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (destroyed): RNA source leukocytes from anonymous pool of non-activated adult donors. Library is oligo-dT primed and directionally cloned (Ecovo site is destroyed upon cloning). Acrage insert size 1.7 kb, insert size range 1.2-3.3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 027. Note: this is a NIH, MGC Library."
                           NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strauberg, Ph.D.

Email: cgapbs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov

Plate: LLAMMIS45 row: K column: ll
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Sukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 913)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="Vector: pCMV-SPORT6; Site_1: Not1; Site_2: EcoRV
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18;
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100.0%; Pred. No. 18;
ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5217154"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone_lib="NIH_MGC_118"
/tissue_type="leukocyte"
/lab_host="DH108"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               High quality sequence stop: 828.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1112 AACAGGCCCTGGGCGGTGGGC 1132
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BF204175
BF204175.1 GI:11097761
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Best Local Similarity 100.0
Matches 21; Conservative
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                                      AUTHORS
TITLE
JOURNAL
COMMENT
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ORIGIN
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BF204175
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/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BE263765 718 bp mRNA linear EST 13.JUL-2000 601194122F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3537940 5',
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EUNATYOTA; MELAZOA; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 718)

NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)

Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
Plate: LLCM222 row: 1 column: 05
Plate: LLCM222 row: 1 column: 05
High quality sequence stop: 649.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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0
                                                                        1.4%; Score 21; DB 17; Length 536;
100.0%; Pred. No. 17;
tive 0; Mismatches 0; Indels
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1.4%; Score 21; DB 10; Length 718;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 21; Consørvative 0; Mismatches 0; Indels
      180
      Б
      81
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                                                                                                                                                                                                                                    916 TGCCCTGTGGGGAGCTGGGAA 936
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BI910102
BI910102.1 GI:16173443
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   119 c
                                                                                                                                                                      21; Conservative
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BE263765
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                                                                                                                                      Best Local Similarity
   156 a
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                                                                                                    Query Match
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KEYWORDS
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ORGANISM
BASE COUNT
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BE263765
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FEATURES

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VERSION

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Gaps . 0

Indels

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7. 962
/organism="Homo sapiens"
/db xref="taxon:9606"
/db xref="taxon:9606"
/clone="IMAGE:6249314"
/clone=lib="MIR_MGC_lid"
/tlasue_lib="MIR_MGC_lid"
/tlasue_lib="MIR_MGC_lid"
/tlasue_lib="MIR_MGC_lid"
/tlasue_lid="ducial carcinoma, cell line"
/tlasue_lid="ducial carcinoma; cell li
                                                                                                                                                                                                                                                                                                                                                                     962 bp mRNA linear EST 15-JUL-2002
AGENCORT_8340711 NIH_MGC_110 Homo saplens cDNA clone IMAGE:6249314
5, mRNA sequence.
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BM563662.1 GI:18810777
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National institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)

Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
Tissue Procurement: ArCC
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM2390 row: j column: 03
High quality sequence start: 3
High quality sequence store: 587.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 962)
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                   Length 953;
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                                                                                                                                                                       729 CGGGAGCGCAACCGCATGCAC 749
                                                                                                                                                                                                             334 CGGGAGCGCAACCGCATGCAC 354
                      Query Match
Best Local Similarity 100.0
Matches 21; Conservative
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TITLE
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               /clone="Index of the content of the 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AU067624 Sugano mouse brain mncb Mus musculus cDNA clone MNCb-3693 5', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. I (bases I to 93).
Hashimoto, K., Kusuda, J., Tanuma, R., Ito, A., Hirata, M., Toyoda, A., Suzuki, Y., Sasaki, M. and Sugano, S.
Isolation of full-length cDNA clones from a mouse brain cDNA Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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National Institute of Infectious Diseases
23-1, Toyama 1-chome, Shinjuku-ku, Tokyo 162-8640, Japan
Email: khashidihi.go.jp
URL: http://www.nih.go.jp/yoken/genbank/.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1.4%; Score 21; DB 12; Length 913; 100.0%; Pred. No. 18; 0; Indels iive 0; Mismatches 0; Indels
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/strain="C57BL"
/cre="taxon:10090"
/clone="MNCb-3693"
/clone=lib="Sugano mouse brain mncb"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Katsuyuki Hashimoto
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/dev_stage="adult"
/lab_host="TOP10"
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KEYRORDS

SOURCE

ORGANISM Human.

DENARYCRASE MEEZOR: Chordata; Craniata; Vertebrata; Buteleostom!; Human.

BURATORISM Homo saplens

REPERBENCE

AUTHORS

NIH-MGC http://mgc.nci.nh.gov/.

AUTHORS

NIH-MGC http://mgc.nci.nh.gov/.

INDAD1816d (1999)

CONTACT: Robert Strausberg, Ph.D.

Email: agaphs remail.inh.gov

Tissue procurement: Arg.E. Consortium (LALL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLML at:

Lond through the I.M.A.G.E. Consortium/LLML at:

Alabolity sequence stop: 654.

Location/Qualifiers

Source

J. 1022

Organism-Homo sapiens"

Alabolost-Public (Adecald And Report Primith)

Anderbord And Source

Adaptor: GGCAGG(G) Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of Galifornia, Berkels) using 2AP-CDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies).

BASE COUNT

177 a 324 c 319 g 202 L
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Search completed: April 8, 2003, 23:14:59
Job time : 2274 secs

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0; Gaps

Query Match 1.4%; Score 21; DB 13; Length 1022; Best Local Similarity 100.0%; Pred. No. 19; Matches 21; Conservative 0; Mismatches 0; Indels

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AJ133776 Homo sapi
AF234829 Homo sapi
AL463311 Human DNA
AC021954 Homo sapi
A91167 Sequence 1
Y10619 R.norvegicu
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AC124395 Mus muscu
U67776 Mus musculu
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AC011010 Home sapi
A7012659 Gallus ga
A7012600 Gallus ga
A7012600 Gallus ga
AF123883 Gallus ga
AF123884 Gallus ga
AF123888 Home sapi
AC011428 Home sapi
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AC023886 Homo sapi
AF303002 Homo sapi
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U94588 Danio rerio
AF024535 Danio rer
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AF234829
AL450311
AC021954
A91167
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AC109783
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-WARN_TIMEOUT-30 -THREADS-1 -XGAPOP-10 -XGAPEXT-0.5 -FGAPOP-6 -FGAPEXT-7
                                                                                  8, 2003, 21:20:34 ; Search time 2813 Seconds (without alignments) 2214.007 Million cell updates/sec
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1127
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GenCore version 5.1.4_p5_4578
Copyright*(c) 1993 - 2003 Compugen Ltd.
                                                         nucleic search, using frame_plus_p2n model
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Maximum Match 100%
Listing first 45 summaries
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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/translation="MTPOPSGAPTVOVTRETERSFPRASEDEVTCPTSAPPSPTRTRG NCAEAEERGCGGAPRRIBHNINSA
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(Dases 1 to 5340)

del Bosque-Plata, L., Lin, J., Horikawa, Y., Schwarz, P.E., Cox, N.J., Iwasaki, N., Ogata, M., Iwamoto, Y., German, M.S. and Bell, G.I. Mutations in the coding region of the neurogenin 3 gene (NEUROG3) are not a commo cause of maturity-onset diabetes of the young in
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442 CGCACACCGGGGAACTGCGCAGAGGCGGAAGAGGGAGGCTGCCGAGGGGCCCCCGAGGAAG 501
                               LeuArgAlaArgArgGlyGlyArgSerArgProLysSerGluLeuAlaLeuSerLysGln
                                                 562 CGACGGAGTCGGCGAAAGAAGGCCAACGACCGCGAGCGCAATCGAATGCACGACCTCAAC
                                                                                                                                                                                                                                                                                                          SerLeuSerProAlaAlaSerLeuGluGluArgProGlyLeuLeuGlyAlaThrSerSer
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7.organism="Homo sapiens"
/db_xref="taxon:9606"
<3022. >3666
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/codon_start=1
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Lin, J. and German, M.
Direct Submission
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NCAEAEEGGCRGAPRKLRARRGGRSRPKSELALSKORRSRRKKANDRERNRMHDLNSA
LDALRGVLPTFPDDAKLTKIETLRFAHNYIWALTQTLRIADHSLYALEPPAPHCGELG
SPGGPPGDWGSLYSPSGASLSPAASLEERPGLLGATSSACLSPGSLAFSDFL"
459 c 413 g 228 t
                PRI 19-JUN-1999
                                                                                                                                                                                                                                                                                 Direct Submission
Submitted (16-WAR-1999) Ravassard P., Lgn, CNRS UMRC 9923, Hopital
de la Pitie Salpetriere, Bat. CERVI, 83 Bd. de l'Hopital, 75013
PARIS, FRANCE
                                                                                                                                                                                                       The human neurogenin 3 homolog maps to chromosome 10q21.3 and its expression pattern is identical to that of its murine counterparts
                                                                                                                         Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo. 1 (bases 1 to 1330)
Rayassard, P., Icard-Liepkalns, C., Wiard, L., Julien, J.P. and
                                                                            bHLH transcription factor; neurogenesis; neurogenin 3; ngn3 gene
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/db_xref="taxon:9606"
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/gene="ngn3"
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JOURNAL Submission Submitted (12-JUL-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 18A, UK. E-mail enquiries: humquery@sanger.ac.uk CB10 18A, UK. E-mail enquiries: humquery@sanger.ac.uk COMMENT on Jul 84, 2001 this sequence version replaced gi:14575291. During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above. This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality) as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em:, EMBL: Sw:, SWISSPROT; Tr:, TREMBL: Wer, WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 10, constructed by the Sanger Centre Chromosome 10	Mapping Group. Further information can be found at http://www.sanger.ac.uk/HGP/Chr10 RP11-34333 is from the library RPCI-11.2 constructed by the group of Pieter de Jong. For further details see http://www.chori.org/bacpac/home.htm VECTOR: pBAces.6 http://www.chori.org/bacpac/home.htm VECTOR: pBAces.6 This sequence is the entire insert of clone RP11-343J3 The true left end of clone RP11-242G20 is at 139955 in this sequence. The true right end of clone RP11-404C6 is at 6588 in this sequence. FEATURES 1. 165110 /Gradion/Qualifiers source /Graganism="Homo sapiens" /Gradion/Chromosome="10"		repeat_region 5062. 5438 repeat_region 6916. 8080 repeat_region 6916. 8080 note="LibbEc repeat: matches 1168. 2367 of consensus" note="LibbEc repeat: matches 15. 184 of consensus" note="Min repeat: matches 55. 184 of consensus" note="Min repeat: matches 55. 194 of consensus" note="Min repeat: matches 55. 194 of consensus" note="Alusx repeat: matches 1. 294 of consensus" repeat_region note="Alusx repeat: matches 1. 294 of consensus" note="Alusx repeat: matches 1. 294 of consensus" repeat_region 12479. 12608 repeat_region 13433. 13876 repeat_region 13433. 13876 note="Min repeat: matches 1. 301 of consensus" note="Min repeat: matches 1. 301 of consensus" note="Alusq repeat: matches 243. 299 of consensus" note="Alusq repeat: matches 243. 299 of consensus"
IDALKGVLPTFPDDAKLTRIETLRFAHNYIWALTOTLRIADHSLYALEPPAPHCGELG SPGGSPGDWGSLSPASGLSPASLEERPGLIGATSSACLSPGSLAFSDFL" ORIGIN	114.2 CGCACACGGGGGAACTGCGCAGAGGGGGAGCTGCCGGAGGGCCCCCGGGGAAGGGGGAGCCCCCGAGGGACCCCCGAGGGAAGAGGGGAAGAGGGGAAGAGGGGAGCCCCCGAGGAAGAGGGGAAGAGGGGAAGAGGGGAAGAGGGGAAGAG	121 LysileGluthrLeuArgPheAlaHisAsnTyrIleTrpAlaLeuThrGlnThrLeuArg	Db 3562 AGCTGAGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGCCACCTTTCC 3521 Qy 201 AlaCysLeuSerProGlySerLeuAlaPheSerAspPheLeu 214

repeat_region	1484314943 /note="MER86 repeat: matches 9109 of consensus"	repeat_region 3921
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	00	repeat_region 55237
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•		Qy 41 ArgThrProGlyAsnC
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L. Submitted (22-JNN-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA

3 (bases 1 to 173341)

Birren, B. Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Barten, B., Linton, L., Boukhgalter, B. Brown, A., Burkett, G., Campopiano, A., Castle, A., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., Dearer, D., Deare, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L., Grand-Plerre, N., Gratt, G., Hagos, B., Heaford, A., Horton, L., Karatas, A., Howland, J.C., Illev, I., Johnson, R., Landers, T., Lehoczky, J., Levine, R., Lieu, C., Liu, G., Locke, K., Macdonald, P., Marquis, N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACO21954 173341 bp DNA linear HTG 24-AUG-2002 Homo sapiens chromosome 10 clone RP11-57E12 map 10, WORKING DRAFT SEQUENCE, 24 unordered pieces.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30025 TGGCACTGGACGCCCTGGCGGTGTCTGCCTCCCAGACGACGCGAAGCTCACC 29966
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   SerAlaLeuAspAlaLeuArgGlyValLeuProThrPheProAspAspAlaLysLeuThr
                                                                                                                                                       29965 AAGATCGAGACGCTGCGCCTTCGCCCACAACTACATCTGGGCGCTGACACTCAAAACGCTGCGC
                                                                                                                                                                                                                                    121 LysIleGluThrLeuArgPheAlaHisAsnTyrIleTrpAlaLeuThrGlnThrLeuArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Birren, B., Linton, L., Nusbaum, C. and Lander, E.
Homo sapiens chromosome 10, clone RP11-57E12
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AC021954.3 GI:7417809
HTG: HTGS_PHASE1; HTGS_DRAFT.
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Meldrim, J., Meneus, L., Mihova, T., Miranda, C., Mlenga, V., Morrow, J., Murphy, T., Naylor, J., Norman, C.H., O'Connor, T., O'Connor, P., Obonnell, P., O'Nell, D., Ollvar, T.M., Ollver, J., Peterson, K., Pierre, N., Pisani, C., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D., Roy, A., Santos, R., Schauer, S., Severy, P., Spencer, B., Stange-Thomann, N., Stolanovic, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Tirrell, A., Travers, M., Trigilio, J., Vosng, G., Zalnoun, J., Zimmer, A., and Zody, M., Wyman, D., Ye, W.J., Direct Submission, J., Zimmer, A. and Zody, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (24-AUG-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA on Apr 5, 2000 this sequence version replaced g1:6984451.

All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)

http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Center: Whitehead Institute/ MIT Center for Genome Research
McPheeters, R.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Center code: WIBS
Web site: http://www.seq.wl.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
Center project name: L5931
Center clone name: 57_E12
Center clone name: 57_E10
C
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Insert size: 171041; sum-of-contigs
Quality coverage: 3.7 in Q20 bases; sum-of-contigs
Quality coverage: 3.8 in Q20 bases; sum-of-contigs
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27386: contig of 3760 bp
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49020; contig of 5185 bp
49120; gap of 100 bp
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32572: cont
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43735: cont
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59644: gap of

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
        clone_end:T7
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/note="assembly_fragment"
89547. .96459 /
/note="assembly_fragment"
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74797. .81326
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117087. .128890
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66395: contig of
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PAT 22-JAN-2000
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                                                                                       2307 others
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Matches:
Conservative:
Mismatches:
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vector_side:right"
12891. .147290
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a 40928 c 40432.g 45501 t
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Sequence 1 from Patent W09827206.
A91167
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97.66%
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                                                        06-MAY-1997
                                                                                                                                                                                                    (bases 1 to 1491)
Ravassard,P., Chatail,F., Mallet,J. and Icard-Liepkalns,C.
Relax, a novel rat bHLH transcriptional regulator transiently
expressed in the ventricular proliferating zone of the developing
                                                                                                                                                            Euteleostom1;
                                                                                                                                                                                                                                                                                                                                                                Submitted (20-JAN-1997) P. Ravassard, CNRS UMR 9923, Bat. CERVI, Hopital de la Pitie Salpetriere, 83 Bd. de l'Hopital, F-75013 Paris, FRANCE
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                                                        1491 bp mRNA linear ROD transcriptional regulator, Relax.
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Sciurognathi; Muridae;
CCATCCTGTCTGCTCCCGGGCACCCTGGTGTTCTCAGACTTCTTG 1100
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166
14
33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /function="transcriptional regulator"
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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    1491
    organism="Rattus norvegicus"

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                                                                                                                  regulator
                                                                                                                                                                                                                                                                                                                                                                                                                                                         /strain-"Wistar"
/db_xref-"taxon:10116"
/clone_lib-"RT-PCR"
459. ,1103
                                                                                                                                                            Chordata;
Rodentia;
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/product="Relax"
                                                                                                                 Relax; transcriptional Rattus norvegicus.
                                                                                                                                                                                                                                                                 central nervous system
                                                                        for
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849.00
83.72%
77.21%
75.33%
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Ravassard, P.
Direct Submission
                                                                                                     GI:2072737
                                                                                                                                                            Eukaryota; Metazoa;
Mammalia; Eutheria;
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                                                                        mRNA
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Y10619.1 GI:2
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ACCESSION
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KEYWORDS
SOURCE
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No.:
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AUTHORS
TITLE
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PGGGSGWGSTXSPYGASLEPFRALEEFPGLQVPSSPSCLLPGTLVFSDFL"
487 c 487 c 483 g 284 t
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                                Corresponding, N.A.
            1 (bases 1 to 1491)
Icard-Liepkalns, C., Mallet, J. and Corresponding, N.A.
Patent: WO 9827206-A 1 25-JUN-1998;
ICARD LIEPKALNS CHRISTINE (FR); MALLET JACQUES (FR)
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166
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Conservative:
Mismatches:
Indels:
                                                                                                                                              /note="unnamed protein product"
                                                                                                                                                                                                                                                                                                                          Length:
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                                                                         Location/Qualiflers
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/organism="Rattus
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BASE COUNT 182 a 274 c 250 g 155 t ORIGIN Alignment Scores: 9.6e-32 Length: 861 Pred. No.: 819.00 Matches: 163 Percent Similarity: 82.33 Conservative: 14 Best Local Similarity: 75.819 Mismetches: 36 Query Match: 10 72.679 Indels: 2 DB: 10 Gaps: 2 US-09-595-947C-10 (1-214) x MMU76208 (1-861) 1-861)	1 MetThrProGluProSerGlyAlaProThrValGlnValThrArgGluThrGluArgSer	51 LeuargalaargargGlyGlyargSerargProLysSerGluLeualaLeuSerLysGln 51 LeuargalaargargGlyGlyargSerargProLysSerGluLeualaLeuSerLysGln 51 LeuargalaargargGlyGlyargSerargProLysSerGluLeualaLeuSerLysGln 53 CTCGCGCCGACGCGGAGGGCGCAACAGGCCCAAGAGTTGGCACTCAGCAACAG 81 ArgArgSerArgArgLysLysAlaAsnAspArgGluArgAsnArgMetHisAspLeuAsn 61 ArgArgSerArgArGLysLysAlaAsnAspArgGluArgAsnArgMetHisAspLeuAsn 62 ArgArgCGGCGCGCGAAGAAGGCCAATGATGGCATGCCATGCAACGTCAAC	0y 101 SerAlaLeuAspAlaLeuArgG1yValLeuProThrPheProAspAspAlaLysLeuThr 120	Oy 161 SerProGlyGlyProProGlyAspTrpGlySerLeuTyrSerProValSerGlnAla 179	RESULT 8 AF364300 LOCUS LOCUS	NISM MUS EUKA MAMM NCE 1 (ORS Lee, and E Regu
Qy 81 ArgargSerArgArgLysLysAlaAsnAspArgGluArgAsnArgMetHisAspLeuAsn 100	QY 141 IlealaAspHisSerLeuTyrAlaLeuGluProProAlaProHisCysGlyGluLeuGly 160	200 SerAlaCysLeuSerProGlySerLeuAlaPheSerAspPheLeu 214 1056 CCATCTGTCTGCTCCGGGCACCTGGTGTTCTCAGACTTCTTG 1100 SULT 7 776208 MMU76208 MMU76208 861 bp DNA linear ROD 05-FEB FINITION MAS musculus neurogenin 3 (ngn3) gene, complete cds.	VERSION U76208 VERSION U76208.1 GI:1815654 KEYWORDS SOURCE MUS musculus. SOURCE Mus musculus Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. REFERENCE 1 (bases 1 to 861) AUTHORS Sommer, L., Ma.Q. and Anderson, D.J. TITLE neurogenins, a novel family of atonal-related bHLH transcription factors, are putathive mammalian neuronal determination genes that reveal progenitor cell heterogeneity in the developing CNS and DNS	Mol. Ceil. Neurosci. 8 (4), 221-241 (1996) 97153555 9000438 2 (bases 1 to 861) Sommer, L., Ma, Q. and Anderson, D.J. Direct Submission Submitted (24-007-1996) Biology 216-76, California Institute of Technology, Howard Hughes Medical Institute, Pasadena, CA 91125, USA On Feb 5, 41997 this sequence version replaced gi:1666911. Location/Qualifiers	source 1. 861 /organism="Mus musculus" /db_xref="taxon:10090" gene	/codon_start=1 /product = neurogenin 3" /protein_id="AAC53029.1" /db_xxef="G1:1666912" /translat_ido="MAPHPLOALTIOVSPETQOPFPGASDHEVLSSNSTPPSPTLIPR DCSAEVGDCRGTSRYLARRGGRNRPKSELALSKORRSRRKANDRERNRMHLNSA LDALRQVLPPFPDDAXLTKIPELFRAHNYINALTQTLRIADBISFYGPEPPVPCGELGS PGGGSNGDWGSIXSPVSQAGNLSPTASLEEFPGLQVPSSPSYLLPGALVFSDFL"

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Direct Submission
Submitted (01-AUG-2000) Lemaigre F.P., Hormone and Metabolic
Research Unit, Louvain University Medical School, Avenue Hippocrate
T5, box 7529, Brussels 1200, BEGGIUM
On Oct 31, 2000 this sequence version replaced gi:1666087.
Location/Qualifiers
1. 5567
/organism-"Mus musculus"
/strain-"sy129"
/db_xref="taxon:10090"
/clone-"lambda GEMIZ clone 19C"
/coll_line-"D3"
                                                                                                                       25-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                    Jacquemin, P., Durviaux, S.M., Jensen, J., Godfraind, C., Gradwohl, G., Guillemot, F., Madsen, O.D., Carmeliet, P., Dewerchin, M., Collen, D., Gousseau, G.G. and Lemalgre, F.P.
Transcription factor heptocyte nuclear factor 6 regulates
pancreatic endocrine cell differentiation and controls expression
                                                                                                                                                                                                                                             Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Mus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Direct Submission
Submitted (04-NOV-1996) G.J. Gradwohl, IGBMC,
CNRS-INSERN-Universite Louis Pasteur, BP163, C.U. de Strasbourg,
FF-67404 ILLKIRCH cedex, FRANCE
Revised by [4]
4 (bases 1 to 5567)
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                     SerAlaCysLeuSerProGlySerLeuAlaPheSerAspPheLeu
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Mol. Cell. Biol. 20 (12), 4445-4454 (2000)
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/protein_id="CAA70366.1"
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Rodentia;
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1923. .5567
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Mammalia; Eutheria; R
1 (bases 1 to 5567)
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Mus musculus
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DCSRAEVGDCRGTSKLRARRGGRNRPKSELALSKORRSRRKKANDRERRNHHINSA
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PGGGSRGMGMGSIXSPVSQAGNLSPTASLEEFPGLQVPSSPSYLLPGALVFSDFL"
560 c 537 g 367 t
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2 (bases 1 to 1861)
Schwitzgebel,V. and German,M.
Direct Submission
Submitted (26-MAR-2001) Hormone Research Institute, Univer
California San Francisco, 513 Parnassus Ave, HSW1090, San
Francisco, CA 94145-0534, USA
Location/Qualifiers
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Mismatches:
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Mus.

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Hazen Genome Sequencing
1 Bungtown Road, Cold Spring
                                                                                                                                                                                                                   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; 1 (bases 1 to 138070)

McCombie,W.**, Baker,'D.**, Balija,V., Dedhia,N.N., de la Mastide,M., Katzenberger,F., Kult,K., King,L., Kirchoff,K.A., Miller,B., Muller,S., Nascimento,L.U., O'Shaughnessy,A.L., Preston,R.K., Santos,L., Spiegel,L.A., Palmer,L., Yang,C. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                            arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                     NOTE: This is a 'working draft' sequence. It currently consists of 17 contigs. The true order of the pleces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                            Insert size: 173000; agarose-fp
Insert size: 14616; sum-of-contigs
Quality coverage: 4.00 in Q20 bases; agarose-fp
Quality coverage: 3.70 in Q20 bases; sum-of-contigs
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g of 9262 bp in length
k unknown length
g of 8901 bp in length
k unknown length
g of 8378 bp in length
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contig of 10669 bp in length
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of 4658 bp in length
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gap of unknown length
contig of 1641 bp in length
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Contact: nccombledcshl.org
                                                                                                                                                           Direct Submission
Submitted (07-FEB-2002) Lita Annenberg
Center, Cold Spring Harbor Laboratory,
Harbor, NY 11724, USA
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of 6449 bp
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                                                                                                  Mouse Genomic Sequence
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/db_xref-"SWISS-PROT:P70661"
/translation="WAPHPLDALTIOVSPETOQPFPGASDHEVLSSNSTPPSFTLIPR
/translation="WAPHPLDALTIOVSPETOQPFPGASDHEVLSSNSTPPSFTLIPR
DCSEAEVOGCGTSRKLRARRGGRNFPKSELALSKORRSRRKKANDRERNRMHNLNSA
LDALRGVLPTFPDDAKLTKTETLRFAHNYIWALTQTLRIADHSFYGPEPPPVFGELGS
PGGGSNGMISPFRALEEFPGLQVPSSPSYLLPGALVFSDFL"
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HTG; HTGS_PHASE1; HTGS_DRAFT
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2 (bases 1 to 185806)
MCPherson, J.D. and Waterston, R.H.
Birect Submission
Submitted (15-JUL-2002) Genome Sequencing Center, 4444 Forest Park
Parkway, St. Louis, MO 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NOTE: This is a 'working draft' sequence. It currently consists of 36 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                           Sequencing vector: plasmid: 100%
Sequencing vector: plasmid: 100%
Chemistry: Dye-primer ET; 0% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 173518 bases at least 030
Consensus quality: 177276 bases at least 030
Consensus quality: 17761b bases at least 030
Insert size: 192000; agarose-fp
Insert size: 184535; sum-of-contigs
Quality coverage: 3.66 in 020 bases; agarose-fp
Quality coverage: 3.85 in 020 bases; sum-of-contigs
                                                                                                                                        Center: Washington University Genome Sequencing Center
Center code: WUGSC
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Mus musculus chromosome UNK clone RP23-459M2, WORKING DRAFT
SEQUENCE, 36 unordered pieces.
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 /db_xref="taxon:10090"
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Matches:
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Db 158824 ATGGCGCTCATCCTTGGATGCGCTCACCATCCAAGTGTCCCCAGAGACACAACAT 158883 DD 158944 CTCATACCTAGGGACTGCTCCGAAGCAGAAGTGGGTGACTGCCGAGGGACCTCGAGGAAG 159003 1 MetThrProGlnProSerGlyAlaProThrValGlnValThrArgGluThrGluArgSer 20 41 ArgThrProGlyAsnCysAlaGluAlaGluGluGlyGlyCysArgGlyAlaProArgLyS 60 // Octa- assembly_name:Contig48" / 8666. '85726 / note-"assembly_name:Contig49" / 8666. '97866 Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps: /note="assembly_name:Contig39" 35421. 38808 /note="assembly_name:Contig40" 38909. 43846 /note="assembly_name:Contig41" 43947. 49171 /note="assembly_name:Contig42" 49272. 53157 /note="assembly_name:Contig44"
57832 . .62660
/note="assembly_name:Contig45"
62761 . .68243
/note="assembly_name:Contig46"
68344 . .73047 /note="assembly_name:Cont1g43" 53258. .57731 US-09-595-947C-10 (1-214) x AC127417 (1-185806) 1.17e-29 819.00 82.33% 75.81% Score:
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Biren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, M.,
Baldwin, J., Barna, N., Beckerly, R., Boguslavkiy, L., Boukhgalter, B.,
Baldwin, J., Barna, N., Beckerly, R., Boguslavkiy, L., Boukhgalter, B.,
Cooke, P., DeArellano, K., Dewar, K., Domino, M., Donelan, L.,
Ferreira, P., FitzHugh, W., Forrest, C., Funke, R., Gage, D.,
Galagan, J., Gardyna, S., Grant, G., Haeford, A., Horton, L.,
Howland, J.C., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J.,
McDacky, J., Lleu, C., Locke, K., Macdonald, P., Marquis, N.,
McDacky, J., McGurk, A., McKernan, R., McLaughiln, J., Maldrim, J.,
Morrow, J., Naylor, J., Norman, C., O'Connor, T., O'Donnell, P.,
Peterson, K., Pollara, V., Riley, R., Roy, A., Santos, R., Severy, P.,
Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J.,
Tesfaye, S., Tirrell, A., Vassiliev, H., Vo, A., Wheeler, J., Wu, X.,
Wwman, D., Ye, W. J., Zimmer, A. and Zody, M., Wheeler, J., Wu, X.,
Direct Submission
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Birren, B., Linton, L., Nusbaum, C. and Lander, E. Homo gaplens, clone RP11-6P16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Db 159361 GGTAACCTGAGGCCCACGGCCTCATTGGAGGAATTCCCTGGCCTGCAGGTGCCCAGGTCC 159420
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SerAlaLeuAspAlaLeuArgGlyValLeuProThrPheProAspAspAlaLysLeuThr 120
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                           Db 159124 TCGGCGCTGGATGCGCTGGCTGCCGGCGCCACCTTCCCGGATGACGCCAAACTTACA
                                                                                                    LysIleGluThrLeuArgPheAlaHisAsnTyrIleTrpAlaLeuThrGluThrLeuArg
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------- Project Information
Center project name: L2916
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Web site: http://www-seq.wi.mit.edu
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This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                  NOTE: This is a 'working draft' sequence. It currently consists of 21 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown.
                                                                                                                                             Insert size: 154000; agarose-fp
Insert size: 168896; sum-of-contigs
Quality coverage: 3.6 in 020 bases; agarose-fp
Quality coverage: 3.3 in 020 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100 bp
f 10146 bp in length
100 bp
f 10674 bp in length
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98864 109919: contig of 11056 bp in length
109920 110019: gap of 100 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5364: gap of 100 bp
141043: contig of 15679 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100 bp
12230 bp in length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11: gap of 100 bp 4638: contig of 617 bp in length 89 gap of 100 bp 4924: contig of 4686 bp in length 24: gap of 100 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     49524: gap of 100 bp
56517: contig of 6993 bp in length
Consensus quality: 114103 bases at least 040 Consensus quality: 141555 bases at least 030 Consensus quality: 158230 bases at least 020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2955 3054; gap of 100 bp 3055 4839; contig of 1785 bp in length 4840 4939; gap of 100 bp 7461; contig of 2522 bp in length
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65413: contig of 8796 bp in length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone_lib-"RPCI-11 Human Male BAC"
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170896: contig of 29753 bp
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4940. .7461
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7562. .11912
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65514 75659; contig of
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1845 2954: cont
2955 3054: gap of
3055 4839: cont
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       86434 86533: gap of 86534 98763: cont
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49424: con
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75760 86433: cont
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us-09-595-947c-10.rge

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                     03-JAN-2001
                                                                                                                                                                                                                                                                                                                 Specification of neurotransmitter receptor identity in developing retina: the chick ATH5 promoter integrates the positive and negative effects of several bHLH proteins
Development 128 (2), 217-231 (2001)
                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
1 (bases 1 to 790)
Matter-Sadzinski,L., Matter,J.M., Ong,M.T., Hernandez,J. and
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Ansermet, 1211 Geneva 4, SWITZERLAND
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                       VRT
                                                                                     AJ012659.1 G1:3892740
atonal protein; bHLH transcription factor; neurogenin.
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104
22
63
43
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Matches:
Conservative:
Mismatches:
Indels:
                       DNA.
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Direct Submission
Submitted (16-NOV-1998) Ballivet M.,
Geneva, 30, qual Ernest Ansermet, 121
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                     790 bp
                          Gallus gallus ngn2/ath4a gene.
AJ012659
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388.50
54.31%
44.83%
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                                                                                                                                                          Gallus gallus
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Best Local Similarity:
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DB:
                     LOCUS
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VERSION
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SOURCE
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AUTHORS
TITLE
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AUTHORS
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GGA012659
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Matches:
Conservative:
Mismatches:
Indels:
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75760, .86433
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86534. .98763
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46.418
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49 AlaGluGluGlyGlyCysArgGlyAlaProArgLysLeuArgAlaArgArgGly 66 	67 GlyArgSerArgProLysSerGluLeuAlaLeuSerLysGln	82 ArgSerArgArgLysLysAlaAsnAspArgGluArgAsnArgMetHisAspLeuAsnSer 101 	102 AlaLeuAspAlaLeuArgGlyValLeuProThrPheProAspAspAlaLysLeuThrLys 121 	122 IleGluThrLeuArgPheAlaHisAsnTyrIleTrpAlaLeuThrGlnThrLeuArg1le 141 	142 AlaAspHisSerLeuTyrAlaLeuGluProProAlaProHisCysGlyGluLeuGly 160 	161 SerProGlyGlyProProGlyAspTrpGlySerLeuTyrSerProValSerGlnAlaGly 180 	181 SerLeuSerProAlaAlaSerLeuGluGluArgProGlyLeuLeuGlyAlaThrSerSer 200 	201 AlacysLeuSerProGlySerLeuAlaPheSer 211	14 00 AF303000 1880 bp DNA 11near VRT 13-NOV-2001 TION Gallus gallus neurogenin 2 gene, complete cds. 10N AF303000.1 GI:11875759 N AF303000.1 GI:11875759		1 (bases 1 tsimmons, A.D., Neurogeninz eprogenitor of Dev. Biol. 2			rce	æ	/codon_ararra_ /product="neurogenin 2" /protein_id="AAG40768.1" /db_xref="G1:11875760"
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ttus norvegicus clone CH230-235Kl0, *** SEQUENCING IN PROGRESS
**, 55 unordered pieces.
/translation="MPVKAESPAPAAEDELLLRLASPAPSASLPSSAGEEDEDEEDG
RPRRLQEGARRAGROBGPPRAARTAETAQRIKRSRRLKANNRERNRHHINAALDALR
BULPTFPEDAKLTKIETLRFAHNYINALIFETLRLAGAARLGGAADAAPGASPSP
ASSWSGGASPAPSZYAGTLSPSPRAGSASDAEHWPPPRGRFAPPPPPHRCL"
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                                                                                                      RS Muzny, D. M., Adams, C., Adlo-Oduola, B., All-osman, F.R., Allen, C., Asta Anaratunge, H.C., Are, J.R., Ayele, M., Barks, T., Barby, D. M., Adams, C., Adlo-Oduola, B., All-osman, F.R., Allen, C., Asta, J.R., Ayele, M., Barks, T., Barban, J.S., Enchola, J., Charez, J., Chen, G., Chen, R., Chen, Z., Chen, Z., Chen, Z., Chen, T., Chilastopoulos, C., Clereland, C.D., Cox, C., Coyle, M.D., Dathorne, S.R., David, R., Davis, C., Davis, C., Eschola, J., Durbin, K.J., Delaney, K.R., Delaney, K.J., Garcia, A., Garner, T., Garza, N., Gill, R., Falls, T., Ferraguto, D., Edag, C.C., Elad, C., Escotto, M., Falls, T., Ferraguto, D., Edag, C.C., Elad, C., Escotto, M., Falls, T., Ferraguto, D., Edag, C., Garcia, A., Garner, T., Garza, N., Gill, R., Harris, C., Harris, K., Harris, K., Harris, K., Harris, K., Harris, K., Haylak, P., Halles, J., Hamilton, K., Harris, K., Harris, K., Haylak, P., Halles, J., Jackson, L.E., Jondson, B., Jacobson, B., B
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Submitted (13-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
On Jul 12, 2002 this sequence version replaced g1:18701957.

Center: Baylor College of Medicine
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                Rattus norvegicus
Eukaryota; Metazda; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
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                  ORGANISM
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SOURCE
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(see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html)
NOTE: This is a 'working draft' sequence. It currently
consists of 55 contigs. The true order of the places
is not known and their order in this sequence record is
arbitrary. Gaps between the contigs are represented as
runs of N, but the exact sizes of the gaps are unknown.
This record will be updated with the finished sequence
as soon as it is available and the accession number will
be preserved.
NOTE: Estimated insert size may differ from sequence length
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55944 GGCTCCAGCCCNTAGCTTCCACTCAGGCNTGTCCGTGCCAGGCCGCAGGAGGCCCCA 56003
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56094 GCGCTGCTGCACTCGCTGCAGAGAGCGTCAAGGCCAAGGCCAACGATCGCGAGCGCAAC 56153 56273 --- CGGCGGCGACGCGAGGTCGCGCGCGGGTGCGGAG 56093 56334 CTCCTGCCTCCGCAGTGTGTCCCCTGC-----CTGCCCGGTCCCCCGAGCCCGGCCAGC_56387 56388 GATACAGAGTCCTGGGGCTCCGGGGCCGCTGCCTCCCCTGCGCTACTGTGGCGTCACCA 56447 115 AspAspAlaLysLeuThrLysIleGluThrLeuArgPheAlaHisAsnTyrIleTrpAla 134 LeuThrGlnThrLeuArgIleAlaAspHisSerLeu-------Tyr 147 148 AlaLeuGluProProAlaProHisCysGlyGluLeuGlySerProGlyGlyProProGly 167 -------LeuTyrSerPro 175 95 ArgMetHisAspLeuAsnSerAlaLeuAspAlaLeuArgGlyValLeuProThrPhePro 114 75 LeuAlaLeuSerLysGlnArgArgSerArgArgLysLysAlaAsnAspArgGluArgAsn 56448 CTCTCTGACCCCAGTAGTCCCTCGGCTTCAGAAGACTTCACCTATGGCCCGGGT 56501 ValSerGlnAlaGlySerLeuSerProAlaAlaSerLeuGluGluArgProGly 193 Asp...-TrpGlySer------135 168 176 56055 QQ g ò g ò g pp g Ω g δ ò δ

Search completed: April 9, 2003, 00:40:21 Job time: 3084 secs

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RESULT 1
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ID AAC61089 standard; DNA; 5340 BP.

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DT 05-FEB-2001 (first entry)
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DT Normal neurogenin 3 (Ngn3) genomic DNA sequence.
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DE Human neurogenin 3; Ngn3; chromosome 10q22.1-22.2; cellular differentiation; XX
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Homo sapiens.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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/SIDS2/gcgdata/geneseq/geneseqn-embl/NA1996.DAT:

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3322 TCGGCACTGGACGCCCTGCGCGGTGTCCTGCCCACCTTCCCAGACGACGCGAAGCTCACC 3381
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                                                                                                                                                                                                                                                                                  SerProGlyGlyProProGlyAspTrpGlySerLeuTyrSerProValSerGlnAlaGly
                                                                                       141 IleAlaAspHisSerLeuTyrAlaLeuGluProProAlaProHisCysGlyGluLeuGly
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transcriptional activity, for targeting expression of genes
central nervous system and treatment of nervous disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA encoding a novel BHLH protein designated RELAX.
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/product= RELAX
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CC protein AAY85617. The Ngn3 gene is located at chromosome position
CC 10q22.1-22.2. The invention relates to the human Ngn3 nucleotide and
CC protein sequences, and includes an antibody recognising the Ngn3 protein.
Also included in the invention is a method for identifying an islet cell
CC precursor, the method involves analysing a cell for the expression of the
Ngn3 gene product, where detection of the product is indicative of an
CC reagent for detecting (in a subject) a predisposition to a defect in
CC pancreatic islet cell function or formation associated with a defect in
CC Ngn3 activity. The Ngn3 protein is useful for identifying beta-cell
C precursor cells expressing Ngn3, and to alter cellular differentiation in
CC mellitus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel human neurogenin 3 polypeptides and polynucleotides encoding them, useful for diagnosis, prevention and treatment of diabetes mellitus and to identify individuals at risk of diabetes -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MetThrProGlnProSerGlyAlaProThrValGlnValThrArgGluThrGluArgSer
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/product- "Ngn3"
/note= "Neurogenin 3"
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                                                                                                          PheProArgAlaSerGluAspGluValThrCysProThrSerAlaProProSerProThr
                                                                                                                                   ArgThrProGlyAsnCysAlaGluAlaGluGluGlyGlyCysArgGlyAlaProArgLys
                                                                                                                                                             LeuArgAlaArgGlyGlyArgSerArgProLysSerGluLeuAlaLeuSerLysGln
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      0 other;
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Matches:
Conservative:
Mismatches:
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      G; 284
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849.00
83.72%
77.21%
75.33%
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      307
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Best Local Similarity:
      BP;
     Sequence 1491
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                  Alignment Scores:
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The Mouse neurogenin 3 is one of several neurogenin proteins discussed in the present invention. The neurogenin nucleic acids can be expressed in a host cell, transformed using an expression vector, to produce recombinant proteins. The proteins and the antibodies raised against the proteins are useful in the study of neurogenesis.
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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                                   5
                                 "Mouse neurogenin
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96US-0030864.
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Best Local Similarity:
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12-NOV-1996;
19-DEC-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Phox2a protein; neuronal subtype-specific marker; growth factor; neurolal differentiation; transplantation; neuronal dysfunction; optical nerve damage, neurodegenerative disorder; neuroprotective; nootropic; anticonvulsant; antiparkinsonian; vulnerary; cerebroprotective; immunesuppressant; antilnfectious; ds.
                                                                                                                                                                                            636
                                                                                                         GlySerLeuSerProAlaAlaSerLeuGluGluArgProGlyLeuLeuGlyAlaThrSer 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Inducing non-neuronal cells to differentiate into neurons and for non-neuronal cells to express a neuronal subtype-specific marker, comprising contacting the non-neuronal cells with a vector containing neurogenin nucleic acid
                        141 IleAlaAspHisSerLeuTyrAlaLeuGluProProAlaProHisCysGlyGluLeuGly
                                                                                   SerPro---GlyGlyProProGlyAspTrpGlySerLeuTyrSerProValSerGlnAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NGN-3; non-neuronal cell; NNC; neurogenesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       neurogenin-3 protein"
                                                                                                                                                                                                                                                       SerAlaCysLeuSerProGlySerLeuAlaPheSerAspPheLeu 214
                                                                                                                                                                                                                                                                                 Murine neurogenin-3 (NGN3) nucleic acid sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Neurogenin-3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Anderson DJ,
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NNCs differentiate into neurons through the recombinant expression of a transcription factor that induces a core program of neurogenesis. Forced expression of murine NGN3 can elicit expression of at least some neuronal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            160
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    636
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              41 ArgThrProGlyAsnCysAlaGluAlaGluGluGlyGlyCysArgGlyAlaProArgLys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       81 ArgArgSerArgArgLysLysAlaAsnAspArgGluArgAsnArgMetHisAspLeuAsn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IlealaAspHisSerLeuTyrAlaLeuGluProProAlaProHisCysGlyGluLeuGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATAGCGGACCACAGCTTCTATGGCCCGGAGCCCCCTGTGCCC---TGTGGAGAGCTGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 180 GlySerLeuSerProAlaAlaSerLeuGluGluArgProGlyLeuLeuGlyAlaThrSer
                                                                                                                                                                                                                                                                                                                                                                     MetThrProGlnProSerGlyAlaProThrValGlnValThrArgGluThrGluArgSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                    PheProArgAlaSerGluAspGluValThrCysProThrSerAlaProProSerProThr
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                                                                                                               other;
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163
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                             BP; 171 A; 263 C; 225 G; 145
                                                                                                                                                                                                                                                                                                                           (1-214) x AAZ51981 (1-804)
                                                                   phenotypic markers even in NNCs.
                                                                                                                                                                      1.27e-42
819.00
82.338
75.818
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                                                                                                                                                                                                                                      Similarity:
                                                                                                                                                                                                                Percent Similarity:
Best Local Similari
                                                                                                           Sequence 804
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                                                                                                                                                       Alignment Scores:
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amino acid sequence, or any of its homologues or orthologues as the reapeutic agents for the treatment of deafness, partial hearing loss, vestibular effects due to damage or loss of inner hair cells, osteoarthritis and abnormal cell proliferation. The invention also encompasses methods of screening for compounds which affect the expression of an atonal associated nucleic acid sequence, in an animal, and a transgenic animal in which an allele of a native atonal associated in activating the atonal associated allele. The nucleic acids or proteins may be used in a method of treating an animal for hearing impairment, joint disease, balance disorders, abnormal cell proliferation, or other disease, to loss of a functional atonal associated nucleic acid or protein. They may particularly be used to treat an animal with a deficiency in cerebellar granule neurons or their precursors, and may and may
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    also be used in promoting mechanoreceptive cell growth and generating hair cells. The present sequence represents an atomal-associated nucleic acid sequence referred to in the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                          Therapeutic use of atonal-associated nucleic acids or amino acids, or any of its homologs or orthologs, for the treatment of e.g. deafness, osteoarthritis and abnormal cell proliferation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      invention relates to the use of atomal-associated nucleic acid or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         e: The present sequence is not shown in the specification, but obtained from GenBank.
cellular proliferation; cerebellar granule neuron; gene therapy; mechanoreceptive cell growth; auditory; osteopathic; cytostatic; transgenic animal; ss.
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                                                                                                                                                                                                                                                                                                                                            Birmingham N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Page -; 142pp; English.
                                                                                                                                                                                                                                                                                                    (BAYU ) BAYLOR COLLEGE MEDICINE
                                                                                                                                                                                                                                        01-JUN-1999; 99US-0137060.
19-JAN-2000; 2000US-0176993.
                                                                                                                                                                                                  01-JUN-2000; 2000WO-US15410.
                                                                                                                                                                                                                                                                                                                                          Zoghbi HY, Bellen H,
                                                                                                                                                                                                                                                                                                                                                                              WPI; 2001-032190/04.
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                                                                                                                   WO200073764-A2.
                                                                                 Mus musculus.
                                                                                                                                                                                                                                          01-JUN-1999;
                                                                                                                                                            07-DEC-2000
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339 40 9 MetThrProGlnProSerGlyAlaProThrValGlnValThrArgGluThrGluArgSer 160 ATGGCGCCTCATCCTTGGATGCGCTCACCAAGTGTCCCCAGAGACACAACCT PheProArgAlaSerGluAspGluValThrCysProThrSerAlaProProSerProThr 861 163 14 36 2 Sequence 861 BP; 182 A; 274 C; 250 G; 155 T; 0 other; Matches: Conservative: Mismatches: Indels: Length: Gaps: US-09-595-947C-10 (1-214) x AAF27266 (1-861) 1.36e-42 819.00 82.33% 75.81% Percent Similarity: *
Best Local Similarity: Alignment Scores: Query Match: Н 21 220 g g ò ð οŽ

Claim 18; Page 49-50; 54pp; English

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160
                                                                                                                                                                    SerPro---GlyGlyProProGlyAspTrpGlySerLeuTyrSerProValSerGlnAla 179
                                                                                                                                                                                                      180 GlySerLeuSerProAlaAlaSerLeuGluGluArgProGlyLeuLeuGlyAlaThrSer 199
                                                                                                                                                                                                                Novel human neurogenin 3 polypeptides and polynucleotides encoding them, useful for diagnosis, prevention and treatment of diabetes mellitus and to identify individuals at risk of diabetes -
LysileGluThrLeuArgPheAlaHisAsnTyrIleTrpAlaLeuThrGlnThrLeuArg
                                                                                                                                     141 IleAlaAspHisSerLeuTyrAlaLeuGluProProAlaProHisCysGlyGluLeuGly
                                                                                                                                             Neurogenin 3; Ngn3; cellular differentiation; diabetes mellitus; islet cell precursor identification; mouse; ds.
                                                                                                                                                                                                                                        Murine neurogenin 3 (Ngn3) genomic DNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                /product= "Ngn3"
/note= "Neurogenin 3"
                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
1093..1737
                                                                                                                                                                                                                                                                                           AAC61090 standard; DNA; 1861 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99US-0128180
                                                                                                                                                                                                                                                                                                                             05-FEB-2001 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2000-664989/64.
P-PSDB; AAY85618.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200059936-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             06-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus
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                                                                                                                                                                                                                                                                                                            AAC61090;
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The human neurogenin 3 Ngn3 DNA sequence AAC61089 encodes the Ngn3 protein AAY85617. The Ngn3 gene is located at chromosome position 10422.1-22.2. The invention relates to the human Ngn3 nucleotide and protein sequences, and includes an antibody recognising the Ngn3 protein. Also included in the invention is a method for identifying an islet cell precursor, the method involves analysing a cell for the expression of the Ngn3 gene product, where detection of the product is indicative of an islet cell precursor. The Ngn3 squence is useful as a diagnostic reagent for detecting (in a subject) a predisposition to a defect in pancreatic islet cell function or formation associated with a defect in
                                                                                                                                                                                                                                                                                                                                      Ngn3 activity. The Ngn3 protein is useful for identifying beta-cell precursor cells expressing.Ngn3, and to alter cellular differentiation in culture in vivo to produce new beta-cells to treat patients with diabetes mellitus. The present sequence represents the murine Ngn3 genomic DNA
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Sequence 1861 BP; 397 A; 560 C; 537 G; 367 T; 0 other;

US-09-595-947C-10 (1-214) x AAC61090 (1-1861)

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MetThrProGlnProSerGlyAlaProThrValGlnValThrArgGluThrGluArgSer 20
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                                                                                          41 ArgThrProGlyAsnCysAlaGluAlaGluGluGlyGlyCysArgGlyAlaProArgLys
                                             21 PheProArgAlaSerGluAspGluValThrCysProThrSerAlaProProSerProThr
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LeuArgAlaArgArgGlyGlyArgSerArgProLysSerGluLeuAlaLeuSerLysGln 80 61 1273 à g

ArgArgSerArgArgLysLysAlaAsnAspArgGluArgAsnArgMetH1sAspLeuAsn 100 SeralaLeuAspalaLeuArgGlyValLeuProThrPheProAspAspAlaLysLeuThr 1333 101 q ò

81

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TCGCCGCTGGATGCGCTGCCGGTGTCCTGCCCACCTTCCCGGATGACGCCAAACTTACA 1452 140 LysileGluThrLeuArgPheAlaHisAsnTyrIleTrpAlaLeuThrGlnThrLeuArg 1393 1453 121 g g ò

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IlealaaspHisSerLeuTyrAlaLeuGluProProAlaProHisCysGlyGluLeuGly 160

141

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1570

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GlySerLeuSerProAlaAlaSerLeuGluGluArgProGlyLeuLeuGlyAlaThrSer 199 180 ò 8

CATCCTATCTGCTCCCGGGAGCACTGGTGTTCTCAGACTTCTTG 1734 SerAlaCysLeuSerProGlySerLeuAlaPheSerAspPheLeu 214 1690 200 ò

Atonal; homologue; orthologue; atonal-associated protein; deafness; hearing impairment; vestibular effect; balance disorder; osteoarthritis; cellular proliferation; cerebellar granule neuron; gene therapy; mechanoreceptive cell growth; auditory; osteopathic; cytostatic; transgenic animal; ss. Math4B) cDNA, SEQ ID NO:4. BP. Mouse atonal homologue 5 (ATOH5, AAF27254 standard; cDNA; 5567 (first entry) WO200073764-A2. Mus musculus 24-APR-2001 07-DEC-2000. AAF27254; AAF27254 RESULT

(BAYU) BAYLOR COLLEGE MEDICINE. 19-JAN-2000; 2000US-0176993. 99US-0137060 01-JUN-1999;

2000WO-US15410

01-JUN-2000;

Ben-Arie Hassan B, ż Birmingham Bellen zoghb1 HY,

WPI; 2001-032190/04. P-PSDB; AAB60350

Therapeutic use of atonal-associated nucleic acids or amino acids, or any of its homologs or orthologs, for the treatment of e.g. deafness, osteoarthritis and abnormal cell proliferation -

Disclosure; Page -; 142pp; English.

amino acid sequence, or any of its homologues or orthologues as therapeutic agents for the treatment of deafness, partial hearing loss, vestibular effects due to damage or loss of inner hair cells, osteoarthritis and abnormal cell proliferation. The invention also encompasses methods of screening for compounds which affect the expression of an atonal-associated nucleic acid sequence in an animal, and a transgenic animal in which an allele of a native atonal-associated gene is replaced by a heterologues nucleic acid sequence, thus inactivating the atonal-associated allele. The nucleic acids or proteins may be used in a method of treating an aminal ich hearing impairment, joint disease, balance disorders, abnormal cell proliferation, or other disease related to loss of a functional atonal-associated or nucleic The invention relates to the use of atonal-associated nucleic acid or precursors, and may also be used in promoting mechanoreceptive cell growth and generating hair cells. The present sequence represents an atonal associated nucle acid sequence referred to in the invention.

Note: The present sequence is not shown in the specification, but protein. They may particularly be used to treat an animal with a deficiency in cerebellar granule neurons or their precursors, am

Sequence 5567 BP; 1271 A; 1549 C; 1564 G; 1183 T; 0 other;

was obtained from GenBank

Alignment Scores:			
Pred. No.:	9.25e-42	Length:	5567
Score:	819.00	Matches:	163
ıt S1m	82,33%	Conservative:	14
Best Local Similarity:	75.81%	Mismatches:	36
Query Match:	72.678	Indels:	7
DB;	22	Gaps:	7

US-09-595-947C-10 (1-214) x AAF27254 (1-5567)

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drug; side effect; cancer; central nervous system; cardiovascular;
gastrointestinal; respiratory system; single nucleotide polymorphism;
SNP; cell differentiation; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Oligonucleotide for detecting cytosine methylation SEQ ID NO 36113
                                                     ArgArgSerArgArgLysLysAlaAsnAspArgGluArgAsnArgMetHisAspLeuAsn
                                                                                                                                                                                                                    LysileGluThrLeuArgPheAlaHisAsnTyrIleTrpAlaLeuThrGlnThrLeuArg
                                                                                                                                                                                                                                                                                                             IlealaaspHisSerLeuTyrAlaLeuGluProProAlaProHisCysGlyGluLeuGly
                                                                                                                                                                                                                                                                                                                          SerPro---GlyGlyProProGlyAspTrpGlySerLeuTyrSerProValSerGlnAla
                                                                                                                                                                                                                                                                                                                                                                              5460 GGTAACCTGAGGCCCCACGCCTCATTGGAGGAATTCCCTGGCCTGCAGGTGCCCAGCTCC
                                                                                                                                                                                                                                                                                      5283 AAGATCGAGACCCTGCGCTTCGCCCACAACTACATCTGGGCACTGACTCAGACGCTGCGC
                                                                                                                                                                                                                                                                                                                                                                                                     GlySerLeuSerProAlaAlaSerLeuGluGluArgProGlyLeuLeuGlyAlaThrSer
MetThrProGlnProSerGlyAlaProThrValGlnValThrArgGluThrGluArgSer
                                                                                                                               LeuArgAlaArgArgGlyGlyArgSerArgProLysSerGluLeuAlaLeuSerLysGln
                                                                                                                                                                                     4923 ATGGCGCCTCATCCCTTGGATGCGCTCACCATCCAAGTGTCCCCAGAGACACAACAT
                                                                                    ArgThrProGlyAsnCysAlaGluAlaGluGluGlyGlyCysArgGlyAlaProArgLys
                                        PheProArgAlaSerGluAspGluValThrCysProThrSerAlaProProSerProThr
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05-SEP-2000; 2000DE-1044543.
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This invention describes a novel method for determining the degree of methylation of a particular cytosine in a motif 5'-cpG-3', present in a genomic sample of DNA. The sample is treated chemically to convert cytosine (C) but not methylated C, to uracil, then part of the genomic cytosine (C) but not methylated to two classes, each with at least one member, of oligonucleotides and/or peptide nucleic acid (PNA) oligomers and the degree of hybridisation to both classes is determined from the mapplicon. From the ratio of labels hybridised to the two classes of oligomers, the degree of methylation is calculated. The method is used: (i) for diagnosis and/or prognosis of side effects of therapeutic drugs and of a wide range of diseases, e.g. cancer, disorders of the central nervous, cardiovascular, gastrointestinal and respiratory systems etc., particularly by detecting mutations or single nucleotide polymorphisms (SNP's); and (ii) for differentiation of cell or tissue methylation status of many C residues to be determined almultaneously. Asgal3410-ABQ54121 represent genomic DNA sequences used to illustrate the method for determining the degree of cytosine methylation described in
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hybridization
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                                                Determining the degree of cytosine methylation in for diagnosis and prognosis, comprises selective hamplicons from chemically treated DNA -
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Best Local Similarity:
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SerAlaLeuAspAlaLeuArgGlyValLeuProThrPheProAspAspAlaLysLeuThr

LeuArgAlaArgArgGlyGlyArgSerArgProLysSerGluLeuAlaLeuSerLysGln 80

CGCACACGAAAAACTACGCAAAAACGAAAAAAAAAACTACCGAAAAACCCCGAAAAA 264

41 323 61 61 263 81 81

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IleAlaAspHisSerLeuTyr 147

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Determining the degree of cytosine methylation in genomic DNA, useful for diagnosis and prognosis, comprises selective hybridization of amplicons from chemically treated DNA
                                                                                                                                 Human; cytosine methylation; 5'-CpG-3'; uracil; cytosine; diagnosis; drug; side effect; cancer; central nervous system; cardiovascular; gastrointestinal; respiratory system; single nucleotide polymorphism; SNP; cell differentiation; ds.
                                                                                                    Oligonucleotide for detecting cytosine methylation SEQ ID NO 36114.
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ABQ49523 standard; DNA; 592 BP.
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05-SEP-2000; 2000DE-1044543
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81 ArgArgSerArgArgLysLysAlaAsnAspArgGluArgAsnArgMetHisAspLeuAsn 100
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                                           PheProArgAlaSerGluAspGluValThrCysProThrSerAlaProProSerProThr
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                                                                          210 TTCCCCAAAACCTCGAAAAACGAAATAACCTACCCCACGTCCGCCCCGCCCCAACCCCACT
                                                                                                                                                                         LeuArgAlaArgArgGlyGlyArgSerArgProLysSerGluLeuAlaLeuSerLysGln
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2000DE-1044543
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US-09-595-947C-10 (1-214) x ABQ49523 (1-592)

592 98 25 0 4 0 0

> Conservative: Mismatches: Indels:

3.8e-24 519.00 83.678 66.678 46.058

> Best Local Similarity: Query Match:

Percent Similarity:

Length: Matches:

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DNA that contains the target C is amplified to form a labeled amplicon.

The amplicon is hybridised to two classes, each with at least one member, of ollgonucleotyldes and/or peptide nucleic acid (PNA) oligomers and/or periodises is determined from the classes of phybridisation to both classes is determined from the classes of oligomers, the degree of methylation is calculated. The method is used: (i) for diagnosis and/or prognosis of side effects of therapeutic drugs and of a wide range of diseases, e.g. cancer, disorders of the central nervous, cardiovascular, gastrointestinal and respiratory systems etc., particularly by detecting mutations or single nucleotide polymorphisms (SNP's); and (ii) for differentiation of cell or tissue types and for investigating cell differentiation. The method allows the methylation status of many C residues to be determined simultaneously.

ABD13410-ABD634121 represent genomic DNA sequences used to illustrate the method for determining the degree of cytosine methylation described in
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Sequence 592 BP; 123 A; 59 C; 187 G; 223 T; 0 other;

592 101 4 37	>
Length: Matches: Conservative: Mismatches:	caps:
6.4e-21 467.00 73.94% 71.13% 41.44%	77
Alignment Scores: Pred. No.: Score: Percent Similarity: Best Local Similarity: Query Match:	

US-09-595-947C-10 (1-214) x ABQ49524 (1-592)

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86 LysLysAlaAsnAspArgGluArgAsnArgMetHisAspLeuAsnSerAlaLeuAspAla 105
                                                                                                                                                                                                                                                                     405 AAGAAGGTTAACGATCGCGAGCGTAATCGAATGTATTAATTTTAATTCGGTATTGGACGTT 464
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                                                                        225 GAAGACGAAGTGATTTGTTTTACGTTCGTTTTAGTTTTATTCGTATACGGGGAAT 284
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ABQ49525 standard; DNA; 592 BP. (first entry) 146 LeuTyr 147 585 TTGTAC 590 12-JUL-2002 ABQ49525; RESULT 11 AB049525 ò 셤

Human; cytosine methylation; 5'-CpG-3'; uracil; cytosine; diagnosis; drug; side effect; cancer; central nervous system; cardiovascular; Oligonucleotide for detecting cytosine methylation SEQ ID NO 36116

methylation of a particular cytosine in a motif 5'-CpG-3', present in a genomic sample of DNA. The sample is treated chemically to convert cytosine (C) but not methylated C, to uracil, then part of the genomic convert cytosine (C) but not methylated C, to uracil, then part of the genomic DNA that contains the target C is amplified to form a labeled amplicon. The amplicon is hybridisation to beptide-nucleic acid (PNA) oligomers and the degree of hybridisation to both classes is determined from the member, of oligomers, the degree of methylation is calculated. The method classes of oligomers, the degree of methylation is calculated. The method is used: (i) for diagnosis and/or prognosis of side effects of therapeutic drugs and of a wide range of diseases, e.g. cancer, disorders of the central nervous, cardiovascular, gastrointestinal and respiratory systems etc., particularly by detecting mutations or single nucleotide polymorphisms (SNP's); and (ii) for differentiation of cell or tissue methylation status of many C residues to be determined simultaneously. ABQ13410-ABQ5421 represent genomic DNA sequences used to illustrate the method of methylation described in the contral contral contral properties. Determining the degree of cytosine methylation in genomic DNA, useful for diagnosis and prognosis, comprises selective hybridization of amplicons from chemically treated DNA gastrointestinal; respiratory system; single nucleotide polymorphism; SNP; cell differentiation; ds. Claim 12; 56pp + Sequence Listing; 56pp; German. ä Berlin K, Guetig the disclosure of the invention. 01-SEP-2001; 2001WO-EP10074. 01-SEP-2000; 2000DE-1043826. 05-SEP-2000; 2000DE-1044543. Olek A, Piepenbrock C, (EPIG-) EPIGENOMICS AG. WPI; 2002-371829/40. WO200218632-A2 Homo sapiens. 07-MAR-2002

592 101 4 37 0 Sequence 592 BP; 223 A; 187 C; 59 G; 123 T; 0 other; Length:
Matches:
Conservative:
Mismatches:
Indels: Gaps: 6.4e-21 467.00 73.94% 71.13% Percent Similarity: Best Local Similarity: Query Match: .. № Score:

(1-592)US-09-595-947C-10 (1-214) x ABQ49525

pGluVa	28 TCGGGTGCGTTTATTGTTTAAGTGATTCGTGAGACGGAGCGGTTTTTTTT
ACGAAGTG .aGluAla	3bB GAAGACGAAGTGATTTGATTTACGTTCGTTTCGTTTTAGTTTTATTCGTATACGGGGGAAT 303 46 CysalaGlualaGluGluGlyGlyCysArgGlyAlaProArgLysLeuArgAlaArgArg 65
AGAGGCGG	
-yArgSerA	66 GlyGlyArgSerArgProLysSerGluLeuAlaLeuSerLysGlnArgArgSerArgArg 85

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24-APR-2001 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Atonal; homologue; orthologue; atonal-associated protein; deafness; hearing impairment; vestibular effect; balance disorder; osteoarthritis; cellular proliferation; cerebellar granule neuron; gene therapy; mechanoreceptive cell growth; auditory; osteopathic; cytostatic;
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                                                                                 126 ArgPhealaHisAsnTyrIleTrpAlaLeuThrGlnThrLeuArgIleAlaAspHisSer 145
69
                                                   LysLysAlaAsnAspArg@luArgAsnArgMetHisAspLeuAsnSerAlaLeuAspAla
                                                                                                                                                        LeuArgGlyValLeuProThrPheProAspAspAlaLysLeuThrLysIleGluThrLeu
                                                                                                                                                                                         Ben-Arie N;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chicken atonal homologue ngn2/ath4a cDNA, SEQ ID NO:20.
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19-JAN-2000; 2000US-0176993.
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also be used in promoting mechanoreceptive cell growth and generating hair cells. The present sequence represents an atonal-associated nucleic acid sequence referred to in the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              47 CCAGGGCCCCCCGACCGCCCGACGGCC---GTCGACCAGCGGCCGCGCCCCCTCTCCCC 103
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ArgSerArgArgLysLysAlaAsnAspArgGluArgAsnArgMetH1sAspLeuAsnSer 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SerProGlyGlyProProGlyAspTrpGlySerLeuTyrSerProValSerGlnAlaGly 180
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----GCCTCGCCCTAC
                                                                     Note: The present sequence is not shown in the specification, but was obtained from GenBank.
                                                                                                                                                                                                              790
104
22
63
43
                                                                                                                                             Sequence 790 BP; 91 A; 351 C; 283 G; 65 T; 0 other;
                                                                                                                                                                                                                                       Matches:
Conservative:
Mismatches:
Indels:
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388.50
54.31%
44.83%
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Best Local Similarity:
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ArgGlyValLeuProThrPheProAspAspAlaLysLeuThrLysIleGluThrLeuArg 126
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                    87 LysAlaAsnAspArgGluArgAsnArgMetHisAspLeuAsnSerAlaLeuAspAlaLeu 106
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transcriptional activator; neuron; pancreas; gastrointestine;
knock-out mouse; transgenic animal; cancer; diabetes; gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ---LeuGluGluArgProGlyLeuLeuGlyAlaThrSerSerAla--------
                                                                                                  50 GluGluGlyGlyCysArg-----GlyAlaProArgLysLeuArgAlaArgGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human neurogenic differentiation protein (NeuroD3) DNA clone 20A1
                                                                              67 GlyArgSerArgProLysSerGluLeuAlaLeuSerLysGlnArgArgSerArgArgLys
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           protein. They may particularly be used to treat an animal with a deficiency in cerebellar granule neurons or their precursors, and may also be used in promoting mechanoreceptive cell growth and generating hair cells. The present sequence represents an atomal-associated nucleic acid sequence referred to in the invention.

Note: The present sequence is not shown in the specification, but was obtained from GenBank.
                                        Atonal; homologue; orthologue; atonal-associated protein; deafness; hearing impairment; vestibular effect; balance disorder; osteoarthritis; cellular proliferation; cerebellar granule neuron; gene therapy; mechanoreceptive cell growth; auditory; osteopathic; cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Therapeutic use of atonal-associated nucleic acids or amino acids, or any of its homologs or orthologs, for the treatment of e.g. deafness, osteoarthritis and abnormal cell proliferation
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                                                                                                                                                                                                                                                                                                                                                                                                              Ben-Arie
    Chicken atonal homologue ngn1/ath4c cDNA, SEQ ID NO:18
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Matches:
Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Page -; 142pp; English.
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                                                                                                                                                                                                                                                                                                                                                                        (BAYU ) BAYLOR COLLEGE MEDICINE.
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19-JAN-2000; 2000US-0176993.
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                                                                                                                    transgenic animal;
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Best Local Similarity:
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                                                                                                                                                                                               WO200073764-A2.
                                                                                                                                                        Gallus gallus.
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4.34e-15
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P-PSDB; AAW71016.
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                                                                                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      07-AUG-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Alignment Scores:
Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               07-AUG-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            06-MAY-1994;
02-NOV-1995;
                                                                                                                                                                                                                              21-OCT-1998
                                                                                                                                                                                                                                                                                                                                                                                                                   US5795723-A
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                                                                                                                                                                                                     AAV42932;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AsnSerAlaLeuAspAlaLeuArgGlyValLeuProThrPheProAspAspAlaLysLeu 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ThrLysileGluThrLeuArgPheAlaHisAsnTyrileTrpAlaLeuThrGlnThrLeu 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ---AGGGGCGCGCCCAATATCTCCCGGGCGTCTGAGGTTCCAGGGGCCACAGGACGACGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               --TyrAlaLeuGluProPro 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ----Trp 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GlnProSer-----GlyAlaProThrValGlnValThrArgGluThrGluArgSer 20
                                                                                                                                       Neurogenic differentiation (NeuroD) genes (AAT74887-94) and proteins (AAW22436-43) from human, mouse and frog have been identified, isolated and sequence. NeuroD polypeptides are tissue-specific basic-helix-loop-helix (BHLH) transcriptional activators involved in neuronal, endocrine and gastrointestinal development. They were discovered by expression cloning and screening assays designed to identify possible bHLH proteins capable of interacting with the protein product of the Drosophila daugherless gene. Novel neuroD2 and neuroD3 genes, related to neuroD1, have been identified. NeuroD nucleic acids can be used to produce NeuroD polypeptides, construction of test cell lines, as probes, in gene therapy, and to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SerAlaProProSerProThrArgThrProGlyAsnCysAlaGluAlaGluGluGluGlyGly 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ------ArgArgGlyGlyArgSerArgProLysSerGluLeuAlaLeuSerLys 79
                                                          Nucleic acid encoding neurogenic differentiation polypeptide -
useful e.g. in regulating neuronal, endocrine and gastrointestinal
development
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GlnArgArgSerArgArgLysLysAlaAsnAspArgGluArgAsnArgMetHisAspLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               153 AlaProHisCysGlyGluLeuGlySerProGlyGlyProProGlyAsp--
                                                                                                                                                                                                                                                                                                                      Sequence 1268 BP; 245 A; 455 C; 344 G; 224 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                               1268
103
18
63
54
 Weintraub HM;
                                                                                                                                                                                                                                                                                                                                                                        Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                               produce transgenic animals as models of disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         54 CysArgGlyAlaProArgLysLeuArgAla-----
                                                                                                                                                                                                                                                                                                                                                                Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-595-947C-10 (1-214) x AAT74891 (1-1268)
                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21 PheProArgAlaSerGluAspGluValThrCys-
 Tapscott SJ,
                                                                                                                  Claim 1; Page 64-65; 81pp; English.
                                                                                                                                                                                                                                                                                                                                                             4.34e-15
378.50
51.05%
43.46%
33.58%
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 Lee JE,
                        WPI; 1997-272117/24.
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Query Match:
DB:
                                        P-PSDB; AAW22440
SM,
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Hollenberg
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The present sequence encodes a protein which is a member of the basic helix-loop-helix (bHLH) protein family, and is designated neurob3. The bHLH genes are a family of genes associated with vertebrate neuronal, endocrinal and gastrointestinal development. The observed pattern of neuroD expression distinguishes subclasses of neuroectodermal tumours. The specification describes a method for the classification of human neuroectodermal tumours. The method comprises measuring, in a tumour sample, expression of at least one basic bHLH gene and identifying the tumour subclass by matching expression to predetermined expression profills for known subclasses. For classifying the tumour as a medulloblastoma, the bHLH gene detected is neuroD1 and neuroD3. The method is used to classify neuroectodermal tumours, and to identify
559 TGCGTCCCTGC-----CTGCCCGGTCCCCCAAGCCCCGCCAGCGGAGTCCTGG 612
                                                                                                                              170 GlySer-----LeuTyrSerProValSerGlnAlaGlySerLeuSerProAlaAla 186
                                                                                                                                                                                         613 GGCTCAGGTGCCGCCGCCGCCTCTCTGACCCCAGTAGCCCAGCGCGCTCCGAA 672
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Basic helix-loop-helix; bHLH; neuroD; neuroectodermal tumour;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA encoding human neuroD3 protein, which is a bHLH protein.
                                                                                                                                                                                                                                                                                                     202
                                                                                                                                                                                                                                                                                                                                                   673 GACTICACCTACCGCCCGGCGACCCTGTTTTCTCCTTCCCAAGCCTGC 721
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     medullablastoma and for prognosis of this as aggressive
                                                                                                                                                                                                                                                                                                          SerLeuGluGluArgProGly-LeuLeuGlyAlaThrSerSerAlaCys
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   classification; medulloblastoma; human; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 11; Columns 61-64; 43pp; English.
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55..768
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/product= neuroD3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAV42932 standard; DNA; 1268 BP
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94US-0239238.
95US-0552142.
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		gser 20	GACC 118	-ProThr 33	CGCT 177	yGly 53	201	63	7	rLys 79	CTCG 318	pLeu 99	.III	sLeu 119	GCTC 438	rLeu 13	ACTG 49	oPro 15	CCAG 558	Trp 169	crec 613	aAla 18	CGAA 67			
		-GlyAlaProThrValGlnValThrArgGluThrGluArgSer		Pr	TATCCGGCTTCCTCACC - GACGAGGAAGACTGTGCCAGACTCCAACAGGCAGCCTCCGCT	Serala Pro Pro Ser Pro Thr Arg Thr Pro Gly Asn CysAla Glu Ala Glu Glu Gly Gly			AGGGGCGCCCCAATATCTCCCGGGCGTCTGAGGTTCCAGGGGCACAGGACGACGAG	AlaLeuSe	CAGGAGAGGCGGCGCGCGCGCGCGCGCGGGTCCGCTCCGAGGCGCTGCTGCTCG	GlnargargSerargargLysLysAlaasnaspargGluargasnargMetHisaspLeu	ATGCACAA	AsnSerAlaLeuAspAlaLeuArgGlyValLeuProThrPheProAspAspAlaLysLeu	SACACCAA	ThrLysIleGluThrLeuArgPheAlaHisAsnTyrIleTrpAlaLeuThrGlnThrLeu	sccaagac	TyrAlaLeuGluProPro			TGCGTCCCCTGCCTGCCCGGTCCCCCAAGCCCCGCCAGCGACGCGGAAGTCCTGG	GlySerLeuTyrSerProValSerGlnAlaGlySerLeuSerProAlaAla	GGCTCAGGTGCCGCCGCCGCCTCCCCGCTGACCCCAGTAGCCCAGCGCCGCCTCCAAA	s 202	2 721	
103 118 63 ' 54		ArgGlu	GCAGCAC		CAACAGO	GluAla			GGGGCA	GluLeu	GAGGCG	JASNArgl	SAACCGC	ProAsp	CCCGAC	AlaLeu	secreta	-TyrAla	SCCCTC	GlyAsp	SAGCGAC	SerLeu	FAGCCCA	erAlaCy	AAGCCIG	
9		nValThr	TGCGCC		CAGACTO	nCysAl≀			AGGTTCCA	oLysse	CCGCTC	ggluAre	CGAGCGG	COThrPh	CTCGTT	rileri	ACATOTGO		CCGGGA	lyProPre	೨೦೦೦೦೮	InAlaGl	ACCCCAG	rhrSerS	CTTCCC	
Matches: Conservati Mismatches Indels: Gaps:	(1-1268)	[hrValG]	ACCTCGAC	ThrCys	SACTGTG	ProGlyAs		Ala	SCGTCTG/	SerArgP	ACGCGGG	AsnAspA	AACGATC	ValLeuP	GTGCTGC	HisAsnT	TACAACT		GGCGGTG	ProGlyG	CCCCCAA	ValSerG	CTCTCTG	uGlyAla	GTTTTCT	
	32	yAlaProThr	ATCTCG	pGluVal	CGAGGAAG	rArgThr		sLeuArg	CTCCCGG	yGlyArg	950055	sLysAla	CAAGGCC	uArgGly	GCGCAGC	gPheAla	crrcecc	n	GCCCGGA	uGlyser	GCCCGGT	rSerPro	CTCCCCG	y-LeuLe	CGACCCT	
378.50 51.05% 43.46% 33.58%	214) x AAV429	G1	GACCTGC	erGluAs	CACC-GA	erProTh	:: :: :	roArgLy	CCAATAT	rgArgGl	9229299	rgArgLy	GGCGCGT	spalate	ACGCACT	hrLeuAr	CGCTGCG	dsserre	AAGGGCT	lyGluLeu	-5	LeuTy	ວອວວອວວ	rgProGl	99000090	
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: nt Similarity: Local Similarity Match:	95-947C-10																				9 TGCGT					,
Score: Percent Simi Best Local S Query Match: DB:	5	4	59	21	119	34	178	54	202	64	259	80	319	100	379	120	439	140	499	153	525	170	613	187	673	
Score Perce Best Query DB:	0S-09	δy	g	οy	qq	δ	g	ογ	g	ογ	q	ò	g	ΟŊ	qq	ογ	g	οy	g	οy	qq	QY	QQ	οy	g	

Search completed: April 8, 2003, 23:23:13 Job time: 260 secs

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Sequence 39, Appl
Sequence 22, Appl
Sequence 22, Appl
Sequence 503, Appl
Sequence 62, Appl
Sequence 3, Appl
Sequence 3, Appl
Sequence 21, Appl
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Sequence 251, Appl
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Sequence 251, Appl
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Sequence 35, Appl
Sequence 27737, A
Sequence 16, Appl
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Sequence 43, Appl
Sequence 17, Appl
Sequence 12, Appl
Sequence 12, Appl
Sequence 15, Appl
Sequence 15, Appl
Sequence 15, Appl
Sequence 17, Appl
Sequence 17, Appl
Sequence 13, Appl
Sequence 65, Appl
Sequence 67, Appl
Sequence 65, Appl
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Patent No. US20020015696A1

GENERAL INFORMATION:
APPLICANT: German, Michael S.
APPLICANT: Lin, Joseph
TITLE OF INVENTION: PRODUCTION OF PANCREATIC ISLET CELLS
TITLE OF INVENTION: AND DELIVERY OF INSULIN
FILE REFERENCE: UCSF-129CIP
CURRENT APPLICATION NUMBER: US/09/817,360
CURRENT FILING DATE: 2001-03-20
PRIOR APPLICATION NUMBER: 09/535,145
PRIOR PILICATION NUMBER: 60/128,180
PRIOR APPLICATION NUMBER: 60/128,180
PRIOR FILING DATE: 1999-04-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-10-004-717-35
US-09-864-761-27737
US-10-004-717-16
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Matches:
Conservative:
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US-09-954-531-982
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US-09-833-381-1305
US-10-004-717-49
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US-09-999-121-7
US-09-999-121-13
US-10-004-717-39
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US-08-722-570-14

US-08-722-570-14

US-08-722-570-14

US-10-004-717-43

US-10-004-717-12

US-10-004-717-15

US-10-004-717-15
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1
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US-09-817-360-1
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                                                         Command line parameters:
-MODEL-frame+_p2n.model -DEV-xlh
-MODEL-frame+_p2n.model -DEV-xlh
-MODEL-frame+_p2n.model -DEV-xlh
-MODEL-frame+_p2n.model -DEV-xlh
-UO-Cgn2_1/USPTO_spool/US09595947/runat_07042003_160406_20125/app_query.fasta_1.391
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-FGAPEXT-7 -YGAPOP=10 -YGAPEXT-0.5 -DELDEXT-7
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Sequence 4, Appli
Sequence 24, Appl
Sequence 3, Appli
                                                                                                          Search time 564 Seconds
(without alignments)
332.826 Million cell updates/sec
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1127
1 MTPQPSGAPTVQVTRETERS......LGATSSACLSPGSLAFSDFL 214
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/cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
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/cgn2_6/ptodata/1/pubpna/US10_PUBCOMB.seq:*
/cgn2_6/ptodata/1/pubpna/US10_PUBCOMB.seq:*
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     GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                          nucleic search, using frame_plus_p2n model
                                                                                                             April 8, 2003, 23:15:09; Search time
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9 US-10-004-717-4
9 US-10-004-717-24
10 US-09-817-360-3
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Maximum Match 100%
Listing first 45 summaries
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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GENERAL INFORMATION:
APPLICANT: ZOGHBI, HUDA Y.
APPLICANT: TANG, QI
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPEUTIC USE CITTLE OF INVENTION: OSTEOARTHRITIS, AND ABNORMAL CELL PROLIFERATION: FILE REFERENCE: P01899054
CURRENT APPLICATION NUMBER: US/10/004,717
CURRENT FILING DATE: 2002-08-16
PRIOR APPLICATION NUMBER: 09/585,645
PRIOR FILING DATE: 2000-06-01
                                                                                                                                                                                                                                                                                             61 LeuargalaargargGlyGlyargSerargProLysSerGluLeualaLeuSerLysGln
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 Length:
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2.34e-70
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Best Local Similarity:
Query Match:
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TYPE: DNA
ORGANISM: Mus musculus
US-09-817-360-3
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Best Local Similarity:
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PRIOR APPLICATION NUMBER: 60/176,993
PRIOR FILING DATE: 2000-01-19
PRIOR PRICATION NUMBER: 460/137,060
PRIOR FILING DATE: 1999-06-01
NUMBER OF SEQ ID NOS: 69
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 24
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                                                                       ) ORGANISM: Mus musculus US-10-004-717-24
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Best Local Similarity:
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TITLE OF INVENTION: PRODUCTION OF PANCREATIC ISL
TITLE OF INVENTION: AND DELIVERY OF INSULIN
FILE REPERENCE: UCSF-129CIP
CURRENT APPLICATION NUMBER: US/09/817,360
CURRENT FILING DATE: 2001-03-20
PRIOR PILING DATE: 2001-03-20
PRIOR APPLICATION NUMBER: 09/535,145
PRIOR APPLICATION NUMBER: 09/535,145
PRIOR APPLICATION NUMBER: 60/128,180
PRIOR FILING DATE: 1999-04-06
NUMBER OF SEQ ID NOS: 19
SEQ ID NO 3
LENGTH: 1861
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Sequence 18, Application US/10004717

Sequence 18, Application US/10004717

Publication No. US20020192665A1

GENERAL INFORMATION:

APPLICANT: ZOGUBL, HUDA Y.

APPLICANT: YANG, OI

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPEUTIC USE OF AN TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPEUTIC USE OF AN TITLE OF INVENTION: OSTEOARTHRITIS, AND ABNORMAL CELL PROLIFERATION

FILE REFERENCE: P01899084

CURRENT APPLICATION NUMBER: US/10/004,717

CURRENT APPLICATION NUMBER: 09/585,645

PRIOR FILING DATE: 2000-06-01

PRIOR FILING DATE: 2000-01-19

PRIOR FILING DATE: 1999-06-01

NUMBER OF SEQ ID NOS: 69

SEQ ID NOS: 89

SEQ ID NOS: 80

SEQ ID NOS: 80
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Best Local Similarity:
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Sequence 20, Application US/10004717

GENERAL INFORMATION:
APPLICANT: ZOGHEL, HUDA Y.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPEUTIC USE OF AN TITLE OF INVENTION: STOCKARD ABNORMAL CELL PROLIFERATION:
TITLE OF INVENTION: OSTEOARTHRITIS, AND ABNORMAL CELL PROLIFERATION TITLE OF INVENTION: OSTEOARTHRITIS, AND ABNORMAL CELL PROLIFERATION TITLE OF INVENTION NUMBER: US/10/004,717
CURRENT APPLICATION NUMBER: US/10/004,717
CURRENT FILING DATE: 2002-08-16
PRIOR PAPLICATION NUMBER: 60/176,993
PRIOR FILING DATE: 2000-01-19
PRIOR APPLICATION NUMBER: 60/176,993
PRIOR FILING DATE: 1999-06-01
NUMBER OF SEO ID NOS: 69
SOFTWARE: PATEORIN VET: 2.1
SEQ ID NO 20.
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Best Local Similarity:
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Db 567 TTGGCTTACAACTACATCTGGĠCCCTCTCGAGACCCTTGGTTTGGCCGAGCAGTGCCTC 626	<pre>Qy 147TyrAlafeuGluProProAlaProHisCysGlyGluLeuGlySerPro 162 </pre>	Qy 163 GlyGlyProProGlyAspTrpGlySerLeuTyrSerPro	Qy 177 SerGinalaGlySerLeuSerProAlaAlaSer	QY 188LeuGluGluArgProGlyLeuLeuGlyAlaThrSerSerAla	Qy 202CysLeuSerProGlySerLeuAlaPheSer 211	RESULT 7 1 Sequence 30, Application US/10004717 1 Sequence 30, Application US/10004717 2 Sequence 30, Application US/10004717 3 GENERAL INFORMATION: 4 TITLE OF INVENTION: 5 TITLE OF INVENTION: 6 TOWER OF INVENTION: 7 TITLE OF INVENTION: 7 TITL	Db 478 AIGTCTCCAGGGGGAGAGAGGAGGAGGAGGAGGAGCTGCGCGGGGGTCCGGGGGT 537 Qy 47

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787 CC-CGGGTCAGACGTGGACTACTGGCAGCCCCACCTCCGGAGAAGCATCGTTATGCGCC 845
                                                                                           LENGTH: 1412
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Publication No. US20020192665A1
GENERAL INFORMATION:
APPLICANT: ZOGHBI, HUDA Y.
APPLICANT: ZOGHBI, HUDA Y.
APPLICANT: YANG, QI
TITLE OF INVENTION: ATONAL ASSOCIATED SEQUENCE FOR DEAFNESS,
TITLE OF INVENTION: ATONAL ASSOCIATED SEQUENCE FOR DEAFNESS,
TITLE OF INVENTION: OSTEOARTHRITIS, AND ABNORMAL CELL PROLIFERATION
FILE REFERENCE: P01899US4
CURRENT APPLICATION NUMBER: US/10/004,717
CURRENT FILING DATE: 2002-08-16
PRIOR FILING DATE: 2000-06-01
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US-09-595-947C-10 (1-214) x US-10-004-717-6 (1-1412)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----ThrArgThrProGlyAsnCys-----
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                                                                                                                                                                                                                                                                Length:
Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                           JS-09-595-947C-10 (1-214) x US-10-004-717-37 (1-1412)
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PRIOR APPLICATION NUMBER: 60/176,993
PRIOR FILING DATE: 2000-01-19
PRIOR APPLICATION NUMBER: 60/137,060
PRIOR FILING DATE: 1999-06-01
NUMBER OF SEQ ID NOS: 69
SOFTWARE: Patentin Ver: 2.1
SEQ ID NO 37
                                                                                                                                                                                                                                                                                 370.50
48.47%
40.46%
32.87%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             47 AlaGluAlaGluGlu----
                                                                                                                                                             TYPE: DNA
CORGANISM: Mus musculus
US-10-004-717-37
                                                                                                                                                                                                                                                                                                  Percent Similarity:
Best Local Similarity:
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115 spAspAlaLysLeuThrLysIleGluThrLeuArgPheAlaHisASnTyrIleTrpAlaL 135
                                                                                                                                                                                                                                                                euThrGlnThrLeuArgIleAlaAspHisSerLeu--------TyrA 148
                                                                                                                                                                                                                                                                                                                                                                                                                                         .-----LeuTyrSerProV 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     797 ATACAGAGTCCTGGGGCTCCGGGGCCGCTGCCTCCCCCTGCGCTACTGTGGCGTCACCAC 856
                           rgMetHisAspLeuAsnSerAlaLeuAspAlaLeuArgGlyValLeuProThrPheProA 115
                                                                                                            euAlaLeuSerLysGlnArgArgSerArgArgLysLysAlaAsnAspArgGluArgAsnA 95
                                                                                                                                                                                                                                                                                                                                                    148 laLeuGluProProAlaProHisCysGlyGluLeuGlySerProGlyGlyProProGlyA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    176 alSerGlnAlaGlySerLeuSerProAlaAlaSerLeuGluGluArgProGly 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             857 TCTCTGACCCCAGTAGTCCCTCGGCTTCAGAAGACTTCACCTATGGCCCGGGT 909
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Flehr, Hobbach, Test, Albritton & Herbert
STREET: Four Embarcadero Center, Suite 3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRING SILIEM.

CURRENT APPLICATION DATA:

CURRENT APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE: 27-SEP-1996

CLASSIFICATION: 5365

ATTORNEY/AGENT INFORMATION:

NAME: SILVA, Robin M.

REGISTRATION NUMBER: 38,304

REGISTRATION NUMBER: 38,304

REGISTRATION NUMBER: A-63902/RFT/RMS

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION 1
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GENERAL INFORMATION:
APPLICANT: Anderson, David J.
APPLICANT: Ma, Qlufu
ITITLE OF INVENTION: NEUROGENIN
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: United States
ZIP: 94111-4187
COMPUTER READABLE FORM:
COMPUTER READABLE FORM:
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                              sp-----TrpGlySer-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (415) 781-1989
(415) 398-3249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              : 738 base pairs
nucleic acid
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-722-570-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Alignment Scores:
Pred No.:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23 ArgAlaSerGlu-----SepGluValThrCysProThr-----SerAlaPro 36
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                                                                                                                          US-08-722-570-12

Sequence 12, Application US/08722570

Publication No.

Publication No.

Publication No.

APPLICANT: Anderson, David J.

TITLE OF INVENTION:

NUMBER OF SEQUENCE: 20

CORRESPONDENCE ADDRESS:

ADDRESSE: Flehr, Hobbach, Test, Albritton & Herbert STREET: San Francisco

CITY: San Francisco

STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 94111-4187
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/722,570
FILING DATE: 27-SEP-1996
CLASSIFICATION: 5365
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Mismatches:
Indels:
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Matches:
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NAME: $11va, Robin M.
REGISTRATION NUMBER: 8 4 304
REFERENCE/DOCKET NUMBER: A 6 5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
TELEFAX: (415) 398-3249
TELEFAX: (415) 398-3249
INFORMATION FOR SEQ ID NO: 12:
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LENGTH: 1527 base pairs
TYPE: nucleic acid
STRANDEDNESS: unknown
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52.97%
45.21%
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Best Local Similarity:
Query Match:
                       204 SerPro 205
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MOLECULE TYPE:
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APPLICATION NUMBER: US/08/722,570
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                                                                                                            104 GGCTACAGCCCCTAGCCTCCACCTCGGGGCTGTCCGTGCCAGCCCGGAGGAGCGCTCCCG 163
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                                                                                                                                                                                                                                                                                                            75 LeuAlaLeuSerLysGlnArgArgSerArgArgLysLysAlaAsnAspArgGluArgAsn 94
                                                                                                                                                                                                                                                                                                                           3 ProGlnProSerGlyAlaProThrValGlnValThrArgGluThrGluArgSerPhePro
                                                                                                                                               23 ArgAlaSer-----GluAspGluValThrCysProThr------SerAlaPro
                                                                                                                                                                                                                      164 CCCTCTCCGGG-GCATCGAATGTTCCCGGTGCCCAGGACGAAGAGCAGGAA------
                                                                                                                                                                                                                                                        55 ArgGlyAlaProArgLysLeuArgAlaArgArgGlyGlyArgSerArgProLysSerGlu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           148 AlaLeuGluProProAlaProH1sCysGlyGluLeuGlySerProGlyGlyProProGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            547 GACACTGAGTCCTGGGGTTCCGGGGCCGCTGCCTCCCCCTGCGCCACTGTGGCATCACCA
                                                                                                                                                                                                  37 ProSerProThr ---- ArgThrProGlyAsnCysAlaGluAlaGluGluGlyGlyCys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      493 CTCCTGCCTCCGCAGTGTGTCCCCTGT-----CTGCCCGGGCCCCCGAGCCCGGGCCAGC
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Suite 3400
  16
66
40
8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
Conservative:
Mismatches:
Indels:
                                                                US-09-595-947C-10 (1-214) x US-08-722-570-13 (1-738)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 168 Asp-----TrpGlySer-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 14, Application US/08722570
Publication No. US20030044887A1
GENERAL INFORMATION:
APPLICANT: Anderson, David J.
APPLICANT: Ma, Qlufu
ITITLE OF INVENTION: NEUROGENIN
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Flehr, Hohbach, Test,
STREET: Four Embarcadero Center,
CITY: San Francisco
STATE: California
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51.83%
44.50%
31.90%
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94111-4187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
Percent Similarity:
Best Local Similarity:
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US-08-722-570-14
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                            Query Match
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102 aLeuAspAlaLeuArgGlyValLeuProThrPheProAspAspAlaLysLeuThrLysIl 122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                497 CCCGGGA-------CAGCACCAGGGGGAAGAGAACAGCCCGCGATGCAGGAG 541
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               142 aAspHisSerLeuTyrAlaLeuGluProProAlaProHisCysGlyGluLeuGlySerPr 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            776 CGACCCAGIGCACCGAICIGCIICCACCCCAGCAGCAGCCAIAIIGGIGCAGGACICCIC 835
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          162 oGlyGlyProProGlyAspTrpGlySerLeuTyrSerProValSerGlnAlaGlySerLe 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    896 CTCCCCGGCCAGC-------CCTGCCAGCTCCACCTCGGACAGTATTGAGTC 940
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3 ProGlnProSerGlyAlaProThrValGlnValThrArgGluThrGluArgSerPhePro 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 380 CCGCGATGAAGAGGACGTGACCTCGCTCCCCTGCTCCGTGACCTCCTTTCCG
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                                                                 REGISTRATION NUMBER: 38,304
REGISTRATION NUMBER: 38,304
REFENDE/COCKET NUMBER: 3-63902/RFT/RMS
TELEPHONE: (415,781-1989
TELEFAX: (415,388-3249
TELEX: (415) 38-3249
TELEX: (910,277299)
TELEX: 910,277299
TELEX: 910,277299
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TELEX: 13,27299
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Matches:
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322.50
54.46%
40.38%
28.62%
27-SEP-1996
N: 5365
       FILING DATE: 27-SEP-1996
CLASSIFICATION: 5365
ATTORNEY/AGENT INFORMATION:
NAME: S11va, Robin M.
                                                                                                                                                                                                                                                                                                      nucleic acid
                                                                                                                                                                                                                                                                                                    TYPE: nucleic actor STRANDEDNESS: unki
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Best Local Similarity:
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TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPEUTIC USE OF AN TITLE OF INVENTION: ATONAL ASSOCIATED SEQUENCE FOR DEAFNESS, TITLE OF INVENTION: ATONAL ASSOCIATED SEQUENCE FOR DEAFNESS, TITLE OF INTERNON: OSTERGARTHRITIS, AND ABNORMAL CELL PROLIFERATION FILE REFERENCE: PO1899UG4 CURRENT PILING DATE: 2002-08-16 PRIOR APPLICATION NUMBER: 09/585,645 PRIOR APPLICATION NUMBER: 09/585,645 PRIOR FILING DATE: 2000-06-01 PRIOR FILING DATE: 2000-06-01 PRIOR FILING DATE: 2000-01-19 PRIOR FILING DATE: 1999-06-01 PRIOR FILING DATE: 1999-06-01 SPIOR FILING DATE: 1999-06-01 SOFTWARE: PALENTH OF SEQ ID NOS: 69 SEQ ID NOS: 69 SEQ ID NO 433
                                                                                                                                                        160 GlySerProGlyGlyProProGlyAspTrpGlySerLeuTyrSerProValSerGlnAla 179
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                                                                                                  622 CAGCTGCACGG-ATCTAC---TTCCACCCAGCAGCCATATTGGTACAGGACTCCTA 677
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Sequence 43, Application US/10004717; Publication No. US20020192665A1
GENERAL INFORMATION:
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30.95%
21.16%
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Best Local Similarity:
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                                                                                                                                                                                                                      & Herbert
                                                                                                                                                                                                                                                SIREET: FOUR EMBACAGGES CENTER, SUITE 3400
CITY: San Francisco
STATE: California
COMPRES: California
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURSETY APPLICATION DATA:
APPLICATION NUMBER: US/08/722,570
FILING DATE: 27-SEP-1996
CLASSIFICATION SASSES
ATTORNEY/AGENT INFORMATION:
NAME: Silva, Robin M.
REFERENCE/DOCKET NUMBER: 38,304
REFERENCE/DOCKET NUMBER: 38,304
REFERENCE/DOCKET NUMBER: A-63902/RFT/RMS
TELEFONDE: (415) 781-1989
TELEFONDE: (415) 781-1989
TELEFAX: (415) 781-1989
TELEFAX: (115) 272-99
INFORMATION FOR SEQ ID NO: 15:
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                                                                                                                                                                                                                    Albritton
Suite 3400
                                                                                                                                 APPLICANT: Ma, Qlufu
TITLE OF INVENTION: NEUROGENIN
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: Flehr, Hohbach, Test,
STREET: Four Embarcadero Center,
                                                Sequence 15, Application US/08722570
Publication No. US20030044887A1
GENERAL INFORMATION:
APPLICANT: Ma, Qiufu
APPLICANT: Ma, Qiufu
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LENGTH: 1277 base pairs
TYPE: nucleic acid
STRANDEDNESS: unknown
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57.298
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                                     US-08-722-570-15
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APPLICANT: ZOCHBI, HUDA Y.

APPLICANT: YANG, QI

ITTLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPEUTIC USE OF AI

TITLE OF INVENTION: ATONAL ASSOCIATED SEQUENCE FOR DEAFWESS,

TITLE OF INVENTION: OSTEOARTHRITIS, AND ABNORMAL CELL PROLIFERATION

FILE REFERENCE: PO1899104

CURRENT APPLICATION NUMBER: U09/585,645

PRIOR PLICATION NUMBER: 09/585,645

PRIOR PLICATION NUMBER: 60/176,993

PRIOR FILING DATE: 2000-06-01

PRIOR PLICATION NUMBER: 60/176,993

PRIOR FILING DATE: 1999-06-01

PRIOR FILING DATE: 1999-06-01

NUMBER OF SEQ ID NOS: 69

SOFTWARE: PATENTIN VET. 2.1
                                                                                                 AsnSeralaLeuAspalaLeuArgGlyValLeuProThrPheProAspAspAlaLysLeu 119
                                                                                                                                                                                                                                                                                                        154 ProHisCysGlyGluLeuGlySerProGlyGlyProProGlyAspTrpGlySerLeuTyr 173
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                                                                                                                                                                                                                                                          -------AlaAspH1s-----SerLeuTyrAlaLeuGluProProAla 153
                                                                                                                                                                                                                                                                         622 GGTCAGGGTGGGGAGGCTGCCCACCACCACAGGTCACCCTACTCCACTTCTACCCACC 681
                                                                                                                                                                                                                               562 CAGCCAACTACAAACTIGGIGGCAGGCIGCITACAGCICAACGCCAGAAGITICCIGAIG 621
                                                                                                                                                                                                                                                                                                                                                            174 SerProValSerGlnAlaGlySerLeuSerProAlaAlaSerLeuGluGluArgProGly 193
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              GTC---AAGTICAGGAGAAAGAAAGTAAIGCGCGCGAGAAGGAACCGGAIGCACCC
                                                             502 AGGATTGGCAAGAGCGGGATCTGCTCACGTTCGTCCAAAACTTATGCAAAGGTCTTTCC
GlnArgArgSerArgArgLysLysAlaAsnAspArgGluArgAsnArgMetHisAspLeu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 8, Application US/10004717 Publication No. US20020192665A1 GENERAL INFORMATION:
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238.50
39.29%
30.95%
21.16%
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Best Local Similarity:
Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SerProValSerGlnAlaGlySerLeuSerProAlaAlaSerLeuGluGluArgProGly 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          638 CAGCCAACTACAAACTTGGTGGCAGGCTGCTTACAGCTCAACGCCAGAAGTTTCCTGATG 697
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ArgSerPheProArgAlaSerGluAsp-----GluValThrCysProThrSerAlaPro 36
                                                                                                        -- ProSerProThrArgThrProGlyAsnCysAlaGluAla 49
                                                                                                                                                                                                                 -----GluGlyGlyCysArgGlyAlaProArg 59
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                                                                                                                                                                                                                                                                       302 GAAGAGGAGGAAGAAGACAGAGAAGAAGATGAGAATGGC----
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TTCTATGAAAGTACCTCCCTGAGTGTGCCAGCCCT
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Job time : 586 secs
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GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
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April 8, 2003, 22:56:59; Search time 1739 Seconds (without alignments) 1993.004 Million cell updates/sec
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OM protein - nucleic search, using frame_plus_p2n model
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                                                                                                                                                                                                                                                                                                                                          16154066 seqs, 8097743376 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
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Command line parameters:
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em_gss_pro: em_gss_hum: em_gss_vrt em_gss_fun: em_estba:* em_esthum:* em_estin:* em_estmu:*
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RESULT 1

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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AK008017	
LOCUS	AK008017 1540 bp mRNA linear HTC 19-JAN-2002
DEFINITION	Mus musculus adult male small intestine cDNA, RIKEN full-length
	enriched library, clone: 2010001M19: atonal homolog 5 (Drosophila),
	full insert sequence.
ACCESSION	AK008017
VERSION	AK008017.1 GI:12841941
KEYWORDS	HTC; CAP trapper.
SOURCE	Mus musculus (strain:C57BL/6J) adult male small intestine cDNA to
	mRNA, clone_lib:RIKEN full-length enriched mouse cDNA library
	clone:2010001M19.
ORGANISM	
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

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Please visit our web site (http://genome.gsc.riken.go.jp/) for
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M., Suni,N., Ishihi,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Wamamoto,R., Matsumoto,H., Sakajuchi,S., Ikegami,T., Kashiwagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y. sequencing pipeline with 384 multicapillary sequencer format General Res. 10 (11), 1757-1771 (2000)
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RIKEN Yokohama Institute; 1-722 Suchiro-cho, Tsurumi.tu, Yokohama, Kanagawa 230-0045, Japan (E-mail:Genome-res@gsc.riken.go.jp, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222,
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Carninci, P. and Hayashizaki, Y.
High efficiency full-length cDNA cloning
Weth. Enzymol. 303, 19-44 (1999)
99279253
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                                                                                                   /organism="Mus musculus"/strain="C57BL/6J"
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241. .885
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Zhao, S., Nierman, W., Feldblyum, T., Malek, J., Shatsman, S., Akinret, B., Levins, M., Mcgann, S., Tsegaye, G., Geer, K., Krol, M., de Jong, P. and Fraser, C.M.
and Fraser, C.M.
Mouse BAC End Sequences from Library RPCI-23
Unpublished (1999)
Other. GSSs: RPCI-23-160018.TJ
Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
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clones are derived from the mouse BAC library RPCI-23. For BAC
library availability, please contact Pieter de Jong
(pleter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/orderingframe.htm)
or from Resea ch Genetics (info@resgen.com). BAC end page:
http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html
Seq primer: T7
Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 593)
                                                                                                                                                                                                       160
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="Organ: Kidney/Brain; Vector: pBACe3.6; Site_1:
                                                                                                                                 SeralaLeuAspAlaLeuArgGlyValLeuProThrPheProAspAspAlaLysLeuThr
                                                                                  IlealaaspHisSerLeuTyralaLeuGluProProAlaProHisCysGlyGluLeuGly
                                                                                                                                                                                                                                       661 ATAGCGGACCACAGCTIGIATGGCCCGGAGCCCCTGIGCCC---IGIGGAGAGCIGGGG
                                                                                                                                                                                                                                                                                                                                              GlySerLeuSerProAlaAlaSerLeuGluGluArgProGlyLeuLeuGlyAlaThrSer
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                                                                                                                                                                                                                                                                                                                                                                                                                                    S93 bp DNA RPCI-23-160G18 TV RPCI-23 Mus musculus , DNA sequence.
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Tel: 301 838 0200
Fax: 301 838 0208
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/strain="C57BL/65"
/db_xref="taxon:10090"
/clone="RPOT-23-160G18"
/clone_lib="RPOT-23"
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/lab_host="DH10B"
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BCORI; Site_2: ECORI; Female C57BL/6J mouse kidney and/or brain genomic DNA was isolated and partially digested with a combination of EcoRI and ECORI Methylase. Size selected DNA was cloned into the pBACe3.6 vector at the ECORI sites. The ligation products were transformed into DH10B electrocompetent cells (BRL Life Technologies).
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Actinopteryg11; Neopteryg11; Teleoste1; Ostariophys1; Cypriniformes
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STR00303 segmentation stage cDNA library Danio rerio cDNA clone
CB260 5' similar to NEUROGENIN 1, mRNA sequence.
BQ169355, GI:20376783
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Expression of the zebrafish genome during embryogenesis (2002)
Unpublished (2002)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GlyGlyProProGlyAspTrpGlySerLeuTyrSerProValSerGlnAlaGlySer 181
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udluproproAlaProHisCysGlyGluLeuGlySerPro 	DEDUIZZ/Y MENA Sequence. BU010277 BU010277. BU010277.1 GI:17364159 EST. Japanese medaka. MUTATORIAS Intipes BUXAYOUA: Metazoa: Chordata; Crania Actinopterygii; Neopterygii: Teleos Acanthomorpha; Acanthopterygii: Per Beloniformes; Adrianichthyidae; Oryle Beloniformes; Adrianichthyidae; Oryle Medaka EST Project in Takeda's lab Innuhishad (2011)	COMMENT Contact: Tadasu Shin-1 Center: For Genetic Resource Information National Institute of Genetics 1111 Yata, Mishina, Shizuoka 411-8540, Japan Tel: 81-559-81-6855 Fax: 81-559-81-6855 Fax: 81-559-81-6855 Fax: 10-532 Location/Qualifiers Source 1.632 //strain-"Horneyzias latipes" //strain-"Horneyzias latipes"	### Add #### Add ### Add ### Add ### Add ### A	Oy 2 ThrProd1n
COMMENT Contact: Thisse B Institut de Genetique et de Biologie Moleculaire et Cellulaire CNRS, INSERM, ULB 1, rue Laurent Fries, BP163, CU de Strasbourg, 67404 Illkirch Cedex 7, France Tel: 33 3 88 65 32 01 Email: thisse@idpmc.u-strasbg.fr Email: thisse@idpmc.u-strasbg.fr EST from a CDNA of a gene whose expression is spatially restricted during embryogenesis. We have established its expression pattern on zebrafish embryos from the gastrula stage to 2 days of development. The corresponding data are available on the zebrafish community database at http://zfin.org/ CDNA library preparation: B. Riggleman. DNA Sequencing Dy:IGBMC sequencing facility. Clone distribution: zebrafish international resource center at the	. = 7, 0	d. No.: d. No.: 327.00 Matches: 84 ncent Similarity: 53.14 Conservative: 53.14 Conservative: 53.14 Mismatches: 65 ery Match: 14 Gaps: 66 -09-595-947C-10 (1-214) x BQ169355 (1-1098)		Db 328 AGGAACGAACCACTGTGAAGAAGAACGACGAAGGCCAACGACGC 387 Qy 92 Gluarasanargmethisaspleuhanserlaleuaspalaleuargglyvalleupro 111

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/dev_stage="embryonic day 14.5 post-fertilization"
/dev_stage="embryonic day 14.5 post-fertilization"
/note="vector: pAmple (sibco); Cloned unidirectionally.
/note="vector: pAmple (sibco); Cloned unidirectionally.
/manniatis); Cloning Technique: CUA Cloning (CloneAmp,
Life Technologies); Average insert size: 18 Kb;
Insertion site: TACGTCCACTGANTCTGAGGG-->. Other
Information regarding entire library may be found at
http://pga.swmed.edu/bata/Libraries/microarray_cdna_librar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EST 20-DEC-2001
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2083-52 Mouse E14.5 retina lambda 2AP II Library Mus musculus CDNA,
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 600)
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                                                                                                                                    564
                              226 ------GGGCAACAGCAAGGAAGCGCCGCCGAGGCCGGGCGCGC
                                                                                                   271 GCGGTCGTGCAGGTGGAAAAAAAAACGGCGGCTGAAGGCTAACGACCGGGAACGGAAC
                                                                                                                                                                                                         AspaspalaLysLeuThrLysIleGluThrLeuArgPheAlaHisAsnTyrIleTrpAla 134
                                                                                                                                                                                                                                                                            135 LeuThrGlnThrLeuArgIleAlaAspH1sSerLeuTyrAla-----LeuGluPro 151
                                                                                                                                                                                                                                                                                                                                                152 ProAla------ProHisCys---GlyGluLeuGlySerProGlyGlyProProGly 167
                                                                                                                                                                                                                                                                                                                                                                                                                     168 AspTrpGlySerLeuTyrSerProValSerGlnAlaGlySerLeuSerProAlaAlaSer 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /db_xref-"taxon:10090"
/clone_lib-"Mouse E14.5 retina lambda ZAP II Library"
                                                                   94
55 ArgGlyAlaProArgLysLeuArgAlaArgArgGlyGlyArgSerArgProLysSerGlu 74
                                                                 75 LeuAlaLeuSerLysGlnArgArgSerArgArgLysLysAlaAsnAspArgGluArgAsn :::
                                                                                                                                                                                                                                                                                                                                                                      188 LeuGluGluArgProGlyLeuLeuGlyAlaThrSerSerAlaCysLeuSerProGlySer
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                                                                                                                                                                                                                                                                                             565 ACGTGG-----AGCCCCAGCGGATCCTCGTCCTCCTCCTCCCCGGCG-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Department of Biochemistry and Molecular Biology University of Texas M.D. Anderson Cancer Center Box 117, f1515 Holcombe Blvd., Houston, TX 77030, USA Fax: 713 790 0329.
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Nucleic Acids Res. 29 (24), 4983-4993 (2001)
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BE780690 11089 bp mRNA 11near EST 20-OCT-2000 601469349F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3872172 5',
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.lln.gov
plate: LLAM9626 row: b column: 13
High quality sequence stop: 692.
Location/Qualifiers
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs r@mail.nih.gov
Tissue Procurement: ATCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                131 TyrileTrpAlaLeuThrGlnThrLeuArgileAlaAspHisSerLeuTyrAla-----
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                                                                                                                                                                                                                                                                                   Gaps:
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BE780690
BE780690.1 GI:10201888
                                  6.67e-15
310.50
58,39%
53.28%
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Alignment Scores:
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GI:7984120

ACCESSION VERGION KEYWORDS AT. SOURCE Life ORGANISM	· · · · · · · · · · · · · · · · · · ·	TEFFRENCE 1 (DASSE AUTHORS ROEST-CK AUTHORS ROEST-CK BENDCL, A BENDCL, A TITLE HUMAN GE TOURNAL UNDUblish REPERFENCE 2 (DASSE	20	33 REFERENCE 362 AUTHORS 362 TITLE AUTHORS	53 386	63 FEATURES SOURCE 443	79 503	99	ALYSLeu 119 Score: Similarity: CAAGCTC 622 Best Local Similarity:	139	Qy 32 ProfhrserA CGAAG 738 Db 533 CCCGCGAACG	yserLeu 172	Qy 68 ArgSerArgP 	Qy 86 LysLysAlaA Db 399 ATGAAAGGA	GSS 18-MAY-2000 Db 339 CTGAGGGCCA'd of clone
/tissue_type="retinoblastoma" /lab_host="DH10B (phage-resistant)" /nab_host="Organ: eye; Vector: pCMV-SPORT6; Site_1: Not1; Site_2: Sall; Cloned unidirectionally. Primer: Oligo Average insert size 1.75 kb. Library constructed by	schnologies." 351 c 337 g 122 t 1 others	1.51e-13 Length: 1039 296.50 Matches: 95 42.234 Conservative: 16 42.224 Mismatches: 66 26.314 Indels: 53 12	947C-10 (1-214) x BE780690 (1-1039) GlnProSerGlyalaProThrValGlnValThrArgGluThrGluArgSer	PheProArgAlaSerGluAspGluValThrCysProThr::: :::	SeralaProProSerProThrArgThrProGlyAsnCysAlaGluAlaGluGluGlyGly	CysArgGlyAlaProArgLysLeuArgAla		GlnArgArgSerArgArgLysLysAlaAsnAspArgGluArgAsnArgMetHisAspLeu 	100 AsnSeralaLeuAspAlaLeuArgGlyValLeuProThrPheProAspAspAlaLysLeu 	ThriyslleGluThrLeuArgPhealaHisAsnTyrIleTrpAlaLeuThrGlnThrLeu 	Arg11eAlaAspHisSerLeuTyrAlaLeuGluProProAlaProHisCysGlyGluLeu	GlySerProGlyAspTrpDroGlyAspTrpGlySerLeu GGCGTACCTGGCTGGCCGACCCCAAGGCCGGCAAAGAAGAAGGGGGAGACTGGGGCAAGGCA	TyrSerProValSerGlnAlaGlySerLeuSerProAlaAlaSerLeu	31y 193 GC 873	1037 bp DNA linear GSS 18-MAY-2000 nigroviridis genome survey sequence T7 end of clone
	7 228 a	Alignment Scores: Pred. No.: Score: Percent Similarity: Percent Similarity: Query Match:	595-947C-10 (1-2 4 GlnProSer :: 244 CAGCCGCCTTG	PheProArgAla ::: TATCCGGCTTCC	SerAlaProProSerProThrArg' TCGGGGCCGCGCGCCGCCCGC	CysArgGlyAla AGGGGCGCG	CAGGAGAGGCGG	GlnArgArgSer CTGCGCAGGAGC	AsnSeralaLeu ::: AACGCGGCCCTG	ThrLysileglu 	ArgileAlaAsp ::: CGCCTGGCGGAT	GlySerProGlyGlyProPro-	TyrSerProValSer :: GCGGGGCCCCGACA	GluGluArgProGly CGGACACGACCAGGC	CNS03VJ9 Tetraodon
	BASE COUNT ORIGIN	Alignment S Pred. No.: Score: Percent Sin Best Local Query Match	US-09-595-9 QY 4 G Db 244 G	Qy 21 F Db 304 T	Qy 34 g Db 363 1	Oy 54 C	Oy 64 Db 444 0	Oy 80 C	Oy 100 P	Oy 120 1 Db 623 P	Oy 140 p	Oy 160 c	Oy 173 7 Db 799 (Oy 189 (RESULT 7 CNSO3VJ9/C LOCUS DEFINITION

sequence.

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mitted (12-APR-2000)
s sequence is a single read and was generated as part of a large s sequence is a single read and was generated as part of a large of clone-end sequencing project of the Tetraodon nigroviridis ome. For more information, please take a look at Location/Qualifiers

p://www.genoscope.cns.fr/Tetraodon.

Location/Qualifiers

1. .1037
/organism="Tetraodon nigroviridis"
/db_zef="texaon:99883"
/clone="10b="G"
/clone="10b="G"
/note="6ch02M23"
/clone="10b="G"
/note="6ch02M23"
/some sequence ID : COBGO62AG12LP1-end : T7"
Johns Survey Sequence.

John Injgroviridis.

John I
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2rollius, H., Jaillon, O., Dasilva, C., Fizames, C., Fisher, C.,
1, L., Billault, A., Quetier, F., Saurin, W., Bernot, A. and
hbach, J.

Perization and repeat analysis of the compact genome of the
serization and retraodon nigroviridis
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Conservative:
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24.67%
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JOURNAL
COMMENT ,
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              124
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                                                                       RESULT 9
BJ030202
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                                                          BJ093114 NIBB Mochii normalized Xenopus early gastrula library Xenopus laevis cDNA clone XL141h09 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /dev_stage="stage 10.5" forte='vector: pBSN3; Site_1: NotI; Site_2: EcoRI; cDNAs /note='vector: pBSN3; Site_1: NotI; Site_2: EcoRI; cDNAs vere olive-dry primed and directionally cloned. Staging according to Nieuwkoop and Faber. Library is subtracted and was constructed by N. Garrett and A.M. Zorn, (Wellome/CR Institute): "arrett and A.M. Zorn, and 204 c 178 g 95 t.
                                                                                                                                                                                                                                1 (bases 1 to 629)
Kitayama, A., Terasaka, C., Mochil, M., Ueno, N., Shin-1, T. and Kohara
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone_lib="NIBB Mochii normalized Xenopus early gastrula
                                                                                                                                                                                   Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24 AlaSerGluAspGluValThrCysProThrSerAlaProProSerProThrArgThrPro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              44 GlyAsnCysAlaGluAlaGluGluGlyGlyCysArgGlyAlaProArgLysLeuArgAla
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           64 ArgArgGlyGlyArgSerArgProLysSerGluLeuAlaLeuSerLysGlnArgArgSer
CGTTTTGCCCACAACTACATCTGGGCTTTGACCGAGACTCTGCGCATGGCCGAT 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            629
63
118
12
4
                                                                                                                                                                                                                                                                        Expressed genes in X. laevis embryo Unpublished (2001) Contact: Tadasu Shin-1 Contert. To Genetic Resource Information National Institute of Genetics Institute of Fara, Majonan Shizuoka 411-8540, Japan Fax: 81-559-81-6856
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /tissue_type="whole embryo"
                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Xenopus laevis"
/db_xref="taxon:8355"
/clone="XL141h09"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (1-629)
                                                                                                                                                                                                                                                                                                                                                                                                  Email: tshini@genes.nig.ac.jp
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-595-947C-10 (1-214) x BJ093114
                                                                                                                     BJ093114.1 GI:17592548
                                                                                                                                                                                                                  Xenopodinae; Xenopus.
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280.00
68.64%
53.39%
24.84%
                                                                                                                                                  African clawed frog.
                                                                                                                                                                       Xenopus laevis
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Best Local Similarity:
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                                                                                                       ACCESSION
VERSION
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AUTHORS
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JOURNAL
COMMENT
                              RESULT 8
BJ093114
                                                                                                                                       KEYWORDS
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/tissue_type="whole embryo"
/tissue_type="whole embryo"
/dev_stage="stage 15"
/dev_stage="stage 15"
/note="vector: pBSRN3; Site_1: Not!; Site_2: EcoRI; cDNAs were oligo-dT prinned and directionally cloned. Staging according to Nieuwkoop and Faber. Library is subtracted and was constructed by N. Garrett and A.M. Zorn,
(Wellcorn Institute).

**A 197 C 165 9 # 19 t
                                                                                                                                                                                                                                                                                        EST 05-DEC-2001
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1 (bases 1 to 595)
Kitayama,A., Terasaka,C., Mochii,M., Ueno,N., Shin-i,T. and Kohara
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Xenopus laevis
Sukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                         595 bp mRNA linear EST 05-DEC-2
BJ030202 NIBB Mochili normalized Xenopus neurula library Xenopus
laevis cDNA clone XL003h03 5', mRNA sequence.
BJ030202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Tadasu Shin-i
Contact: Tadasu Shin-i
Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6855
Fax: 81-559-81-6855
Fax:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24 AlaSerGluAspGluValThrCysProThrSerAlaProProSerProThrArgThrPro 43
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     83
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ThrLeuArgPheAlaHisAsnTyrIleTrpAlaLeuThrGlnThrLeuArgIle 141
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Matches:
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source
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JOURNAL
COMMENT
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AUTHORS
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KEYWORDS
SOURCE
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                                                                                                                                                           AL54071 LTL_FL013_FBrn1 Homo sapiens cDNA clone CSODF035YD19 5
AL540071 GI:12869886
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Homo saplens"
/db_xref="taxon:9606"
/clone="cSODF0575D19"
/clone=llb="LTI_F1013_FBrn1"
/dev_stage="pooled tissue from post conception fetuses (20
/lab_lost="DH108"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="Organ: Fetal brain; Vector: pCMVSFORT 6; 1st strand colb was primed with a NotLoilyo(df) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  pcMVSPORT 6 vector. Library was constructed by Life Technologies. Contact: Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville. Maryland 20850, USA Fax: (1) 301 610 8371 Email: Hilangelifetech.com URL: http://fullength.invitrogen.com, 3 others
                                                                                                                                                                                                                                                                                               Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
               104 AspAlaLeuArgGlyValLeuProThrPheProAspAspAlaLysLeuThrLysIleGlu 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         359 TGCTGCTCGGATCGGCCTCCCCCCCCCTTGGCGGCCCTGACCCCCGCTGTCATCCAGCGCCG 418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           419 ACGAAGAAGAAGAAGGAGGAGGAGCCGGCGCGTCAGGGCGGGGGGGCGCGCGGGGGCGCGGGGGC 478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             479 TTA---NGCCGGGCAANGGGGCGCGCGGGCGTTGCTGCGGGGTGCGGAGGGCTGCCGG 535
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                                                                                                                                                                                                                                                                                                                                                                                               Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqrefégenoscope.cns.fr, Web : www.genoscope.cns.fr.
                                                              ThrLeuArgPheAlaHisAsnTyrIleTrpAlaLeuThrGlnThrLeuArg 140
                                                                              CysProThrSerAlaProProSerProThrArgThrProGlyAsnCys-
                                                                                                                                                                                                                                                                                                                                                Li,W.B., Gruber,C., Jessee,J. and Polayes,D. Full-length cDNA libraries and normalization Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length:
Matches:
Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1.78e-11
268.50
51.01%
42.95%
23.82%
                                                                                                                                                                                                                                                                                                                                (bases 1 to 804)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               804
                                                                                                                                                                                                                                                                                 Homo sapiens
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Best Local Similarity:
Query Match:
DB:
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KEYWORDS
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                                                                                                                                                                              DEFINITION
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AUTHORS
TITLE
JOURNAL
                                                              124
                                                                                                                             RESULT 10
AL540071
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/iissue_iype="looyte (stages 5 and 6)"
/lab_host="veroryte (stages 5 and 6)"
/lab_host="rop-10 F'"
/note="veroryte paluescript SK-; Site_1: EcoRI; Site_2:
/note="veroryte paluescript SK-; Site_1: EcoRI; Site_2:
XhoI; cDNA was prepared from 2ug of poly A+ RNA.
ECORI-XhoI cut cDNA was then ligated into Unizap-XR
(Stratagene) with EcoRI at the 5' end and XhoI at the 3'
end. SS-library phagemids were prepared by mass excision
from the original library and normalized by hybridization
to blotinylated driver (prepared from the same library by
PCR) to Cot-onega of II. After removal of hybrids and
excess driver by streptuavidin sepharose chromatography,
the ss-phagemids were made double stranded and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Amopodinae; Xenopus.

1 (bases 1 to 401)

Clifton,S., Johnson,S.L., Blumberg,B., Song,J., Hillier,L., Pape,D.

Amrtin,J., Wylle,T., Underwood,K., Theising,B., Bowers,Y., Person

B., Gibbons,M., Harvey,N., Ritter,E., Jackson,Y., McCann,R.,
Wash Kanopus EST project, 1999

Unpublished (1999)

Contact: Sandy Clifton, Ph.D.

Wash Kanopus EST project, 1999

Wash Kanopus EST project, 1999

Wash Kanopus EST project, 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   da02h12.yl Xenopus laevis oocyte Xenopus laevis cDNA clone XENOPUS_SOURCE_ID:xlnoc001h24 5' similar to gb:gb|U6779.1|xLU67779 AM147434
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Library normalized by Jihwan Song
Library normalized by Jihwan Song
DNA Sequencing DNA Sequencing Center
DNA Sequencing Washington University Genome Sequencing Center
Clone distribution: Xenopus clone distribution information for
this library can be found through Research Genetics, visit their
web page at: http://www.resgen.com/
Seq primer: -40RP from Gibco
High quality sequence stop: 264.
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Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
                                                                                                                                                      655
                                                                                                                                                                                                                                                                                        715
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Fax: 314 286 1810
596 GTCTCCCGAGGCGCCCAAGACGGCCGAGACGCTGCAGCGCCATCAAGAAGACCCGTAGACTG
                                                                                                                                                                                                                          LysAlaAsnAspArgGluArgAsnArgMetHisAspLeuAsnSerAlaLeuAspAlaLeu
                                                                                                                                                                                                                                                                                                                                                         107 ArgGlyValLeuProThrPheProAspAspAlaLysLeuThrLysIleGluThrLeuArg
                                                                                               -----ArgArgSerArgArgLys
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/db_xref="taxon:8355"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PheAlaHisAsnTyrIleTrpAlaLeu 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TTCGCCCACACTACATCTGGGGGACTC 805
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                                                                                            LeuSerLysGln------
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/db_xref="taxon:7719"
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Ciona intestinalis
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Best Local Similarity:
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DB:
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AUTHORS
TITLE
JOURNAL
COMMENT
                                                                                                                                           Pred. No.:
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VERSION
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AV995230
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                                                                                    BASE COUNT
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SOURCE
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                                                                                                ORIGIN
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AV673464 AV673464
AV673464
AV673464.
GI:10111463
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I (basea; Latou,Y.) Kohara,Y. and Shin-i,T.

Expressed genes in Clona intestinalis
Contact: Nori Satch
Department of Zoology
                               6
electroporated into Top-10 F', Original library contruction by Bruce Blumberg (Blumberg et al., 1991 Science*253, 194-196; Hawlet et al., 1995, Genes Dev. 2923-2935). Normalized by Jihwan Song (Song, Cho and Blumberg, unpublished). Note: This is a Xenopus Gene Collection (XGC) library."
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                                                                                                                                                                                                                                                               82 ArgSerArgArgLysLysAlaAsnAspArgGluArgAsnArgMetH1sAspLeuAsnSer
                                                                                                                                                                                                                                                                             2 AAAACCCGGCGCGTTAAAGCCAATAACCGCGAGAAATGGCATGCACCACCTGAACTAT
                                                                                                                                                                                                                                                                                                                                      142 AlaAspHisSerLeuTyrAlaLeuGluProProAlaProHisCysGlyGluLeuGlySer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   162 ProGlyGlyProProGlyAspTrpGlySerLeuTyrSerProValSerGlnAlaGlySer
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Matches:
Conservative:
Mismatches:
Indels:
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sakyo-ku, Kyoto, Kyoto 606-8502,
Tel: 81-75-753-4081
Fax: 81-75-705-1113
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                                                                                                                                        9.97e-12
267.50
58.73%.
49.21%
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Clona intestinalis
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Best Local Similarity:
                                                                                     87
                                                                                                                                                                                                 Query Match:
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KEYWORDS
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ORGANISM
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AVY95230 AVY95230 Nori Satoh unpublished cDNA library, tallbud embryo Ciona AVY95230 Nori Solone citb40g24 5', mRNA sequence.
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/db_xref="taxon:7719"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           158 CATGITITICCGACCTACCCGAGAGAGAATTAACAAAATCGAAACCTIGGGATTC 217
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/db_xrel= cax.....
/clone=lib="Nor! Satch unpublished cDNA library"
/clone=lib="Nor! Satch unpublished cDNA library"
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/dev_stage="tailbud"
/note="vector: pBluescript SK"
* 146 c 117 g 120 t
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1 (Dases 1 to 490)
Satoh, N. Satou, Y., Kohara, Y. and Shin-1, T. Expressed genes in Ciona intestinalis Unpublished (2000)
Contact: Nori Satoh
Department of Zoology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 218 GCATACAATTATATTTGGTGTTTGAGTGAAATGTTAAAA 256
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Mismatches:
Indels:
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Sakyo-ku, Kyoto, Kyoto 606-8502, Japan
Tel: 81-75-753-4081
Fax: 81-75-705-1113
Email: satch@ascidian.zool.kyoto-u.ac.jp.
Location/Qualifiers
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/dev_stage="tailbud embryo"
/note="Vector: pBluescript SK"
125 c 95 g 99 t
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Matches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: cgapbs-remail.nl.gov
Tissue Procurement: Dr. James Lin, Univeristy of Iowa
Tissue Procurement: Dr. James Lin, Univeristy of Iowa
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                   127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 (bases 1 to 814)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                                 ArgSerArgProLysSerGluLeuAlaLeuSerLysGlnArgArgSerArgArgLysLys
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113
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Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                           Length:
Matches:
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Contact: Robert Strausberg, Ph.D.
                                                                                                    Gaps:
                                                                                                                           US-09-595-947C-10 (1-214) x AV995230 (1-490)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                3.48e-10
249.00
80.82%
63.01%
22.09%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Seq primer: pYX-5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       house mouse,
                                                                          Similarity:
                                                             Percent Similarity
Best Local Similar:
                         Scores:
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DB:
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LOCUS
DEFINITION
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                         Alignment
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AUTHORS
TITLE
JOURNAL
COMMENT
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KEYWORDS
SOURCE
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ORIGIN
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ligated with EcoR I adaptor, digested with Not I, and then cloned directionally into pYX-Asc vector. The library tag sequence located between the Not I site and the polyA tail, is GTGCGTGGAA. This library was created for the University of Iowa Mouse Brain Molecular Anatomy Project (BMAP): 'Gene Discovery in the Developing Mouse Nervous System', supported by National Institutes of Mental Health (NIMM), Hemin Chin, Ph.D., program coordinator."
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Matches:
Conservative:
Mismatches:
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Tetraodon nigroviridis.
Tetraodon nigroviridis
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us-09-595-947c-10.rst

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Object Submission
Submitted (12-APR-2000)
Submitted (12-APR-2000)
This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.

Location/Qualifiers
                                        Human gene number estimate provided by genome wide analysis using Tetraodon nigroviridis DNA sequence Jnpublished
                                                                                         2 (bases 1 to 1003)

Roest-Crollius, H., Jaillon, O., Dasilva, C., Fizames, C., Fisher, C.,
Bouneau, L., Billault, A., Quetier, F., Saurin, W., Bernot, A. and
Weissenbach, J.
Charaterization and repeat analysis of the compact genome of the
freshwater pufferfish Tetracdon nigroviridis
Roest-Crollius, H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C., Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F., Saurin,W. and Welssenbach,J.
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274 c 314 g 236 t 7 others
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Ravassard, P.
Direct Submission
Submitted (20-JAN-1997) P. Ravassard, CNRS UMR 9923, Bat. CERVI,
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                    TGGAGGAGTTCCCTGGCCTGCAGGTGCCCAGCTCCCCATCCTGTCTGCTCCGGGCACCC
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GTGTCCTGCCCACCTTCCCGGATGACGCCAAACTTACAAAGATCGAGACCCTGCGCTTCG
                                                                             CCCACAACTACATTTGGGCACTGACTCAGACGCTGCGCATAGCGGACCACAGCTTCTACG
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    1491
/organism="Rattus norvegicus"
/strain="Wistar"

                                                                                                                                                              Score 1460; 1
Pred. No. 0;
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83
Pitie Salpetriere,
                                         /db_xref-"taxon:10116"
/clone_lib="RT-PCR"
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Sciurognathi; Muridae; Murinae;
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                    CCCACAACTACATTTGGGCACTGACTCAGACGCTGCGCATAGCGGACCACAGCTTCTACG
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Mammalia; Eutheria;
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HTG: HTGS_PHASE1.
Rattus norvegicus.
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Center clone name: 920-259G16
Sequencing vector: Plasmid;
Chemistry: Dye-terminator Big Dye: 100% of reads
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                             58240
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Sommer,L., Ma.O. and Anderson,D.J.
Direct Submission
Submission
Submission
Submission
Submission
Submission
Submitted (24-OCT-1996) Biology 216-76, California Institute of
Technology, Howard Hughes Medical Institute, Pasadena, CA 91125,
GCGCTGGATGCGCTGCGCGGTGTCCTGCCCACCTTCCCGGATGACGCCAAACTTACAAAG 821
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100.0%; Pred. No. 1.5e-42;
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nmer, L., Ma, Q. and Anderson, D.J.
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/db_xref-"taxon:10090"
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/note="NGN3"
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/gene="ngn3"
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/gene="ngn3"
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Submitted (01-AUG-2000) Lemaigre F.P., Hormone and Metabolic Research Unit, Louvain University Medical School, Avenue Hippocrate 75, box 7529, Brussels 1200, BELGIUM On Oct 31, 2000 this sequence version replaced g1:1666087.

Location/Qualifiers
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LADLRGVLPPFPDDAKLTKIETLRFAHNYIWALTQTLRIADHSFYGPEPPYPCGELGS
PGGGSRGMGSISFYGAGRALSPTASLEEFPGLQVPSSPSYLLPGALVFSDFL"
1149 c 11564 g 1183 t
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Jacquemin, P., Durviaux, S.M., Jensen, J., Godfraind, C., Gradwohl, G., Guillemot, F., Madsen, O.D., Carmellet, P., Dewerchin, M., Collen, D., Rousseau, G.G. and Lemaigre, F.P.
Transcription factor hepatore nuclear factor 6 regulates
pancreatic endocrine cell differentiation and controls expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /cell_type="embryonic stem cells"
/clone_lib="Genomic library No.62, MboI partial digests
cloned in BamHI"
                                                                                                                                                                                                                                          Submitted (04-NOV-1996) G.J. Gradwohl, IGBMC,
CNRS-INSERM-Universite Louis Pasteur, BP163, C.U. de Strasbourg,
F-67404 ILLKIRCH cedex, FRANCE
Revised by [4]
4 (bases 1 to 5567)
Lemaigre, F.P.
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Mol. Cell. Biol. 20 (12), 4445-4454 (2000)
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/clone="lamba GEM12 clone 19C"
/cell_line="D3"
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/db_xref="GI:1666088"
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3692
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/gene="MATH4B"
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Matches 92; Conservative
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Direct Submission
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      AUTHORS
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LDALRGVLPTFPDDAKLTKIETLRFAHNTIWALTOTLATADHSFYGPEPPVPCGELGS
PGGGSNGDWGSTYSPYGAGNISPTASLEEFPGLQVPSSPSYLLPGALVFSDFL"
560 c 537 g 367 t
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                                                              ROD 03-MAY-2001
                                                                                                                                                                                                                                                               Lee J., Smith, S., Watada, H., Lin, J., Scheel, D., Wang, J., Mirmira, R. and German, M.
                                                                                                                                                                                   Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 1861)
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Cau, E., Gradwohl, G., Fode, C. and Guillemot, F.
Mashi activates a cascade of bHLH regulators in olfactory neuron
                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (26-MAR-2001) Hormone Research Institute, University of California San Francisco, 513 Parnassus Ave, HSW1090, San Francisco, CA 94145-0534, USA Location/Qualifiers
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                                                                                                                                                                                                                                                                                                Regulation of the pancreatic pro-endocrine gene neurogening Diabetes (2001) In press C theses to 1861) Schwitzgebel V. and German, M. Direct Submission
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house mouse.
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/protein_id="AAK50058.1"
/db_xref="GI:13937129"
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/organism="Mus musculus"
/db_xref="taxon:10090"
<1093. .>1737
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                                                                1861 bp
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Mus musculus neurogenin 3
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AF364300.1 GI:13937128
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Y09167
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AC127417

Mus musculus chromosome UNK clone RP23-459M2, WORKING DRAFT
SEQUENCE, 36 unordered pieces.
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Submitted (15-JUL-2002) Genome Sequencing Center, 4444 Forest Park
Parkway, St. Louis, MO 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 185806)
MCPherson, J.D. and Waterston, R.H.
The sequence of Mus musculus clone
Unpublished
                                                                                                                                                                                                                                                                                                                                                                              Db 110917 GCGTGGATGCGCTGCGCGGTGTCCCCGCATCCCCGGATGACGCCAAAG 110858
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Center code: WUGSC
                                                                                                                                                                                                                                                                       Length 138070;
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Insert size: 184535; sum-of-contids
Ouality coverage: 3 66 in 020 bases; agarose-fp
Quality coverage: 3.85 in 020 bases; sum-of-contigs
                                                                                                                                                                                                            1425 others
                                       bp in length
length
bp in length.
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Sequencing vector: plasmid; 100%
Chemistry: Dye-primer ET; 0% of reads
Chemistry: Dye-primer ET; 0% of reads
Chemistry: Dye-terminator B19 Dye; 100% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 173518 bases at least 040
Consensus quality: 177276 bases at least 030
Consensus quality: 179611 bases at least 020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Web site:http://genome.wustl.edu/gsc/index.shtml
Contact: submissions@watson.wustl.edu
      in length
                                                                                                                                                                                                                                                      DB 2; Leny
1. 1.2e-42;
0;
                       length
132682: contig of 4354 bg
132770: gap of unknown le
136341: contig of 3571 bg
136429: gap of unknown le
138070: contig of 1641 bg
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McPherson, J.D. and Waterston, R.H.
                                                                                                                                             /organism "Mus musculus"
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                                                                                                                                                                   /db_xref="taxon:10090"
/clone="RP23-121F10"
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HTG; HTGS_PHASE1; HTGS_DRAFT.
                                                                                                      Location/Qualifiers
1. .138070
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                                           132771
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AC127417
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Submitted (OrFEB-2002) Lita Annenberg Hazen Genome Sequencing
Center, Cold Spring Harbor Laboratory, 1 Bungtown Road, Cold Spring
Harbor, NY 11724, USA
                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutherla; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 138070)
McCombie,W.R., Baker,J.P., Balija,V., Dedhia,N.N., de la Bastide,M., Katzenberger,F., Kuit,K., King,L., Kirchoff,K.A., Miller,B., Muller,S., Nascimento,L.U., O'Shaughnessy,A.L., Preston,R.R., Santos,L., Spiegel,L.A., Palmer,L., Yang,C. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Center: Lita Annenberg Hazen Genome Center, Cold Spring Harbor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NOTE: This is a 'working draft' sequence. It currently consists of 17 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
      musculus clone RP23-121F10, WORKING DRAFT SEQUENCE, 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17785: contig of 17785 bp in length 17874: gap of unknown length 30356: contig of 12482 bp in length 30444: gap of unknown length 42306: contig of 11862 bp in length 42394: gap of unknown length 53598: contig of 11204 bp in length 53586: gap of unknown length 64355: contig of 10669 bp in length 64443: gap of unknown length 74016: contig of 5733 bp in length 74016: contig of 9573 bp in length 74104: gap of unknown length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Insert size: 17300; agarose-fp
Insert size: 141616; sum-of-contigs
Quality coverage: 4.00 in Q20 bases; agarose-fp
Quality coverage: 3.70 in Q20 bases; sum-of-contigs
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6: contig of 9573 bp in length
1: gap of unknown length
5: contig of 9262 bp in length
5: gap of unknown length
6: gap of unknown length
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of 8901 bp in length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Center code: CSHL
Web site: http://www.cshl.org/genseq
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HTG; HTGS_PHASE1; HTGS_DRAFT.
Mus musculus.
Mus musculus
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McComble, W.R.
                                                                                                                                                                                                                                                                                                                       Mouse Genomic Sequence
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but the exact sizes of the gaps are	162344 162443: gap of unknown length
	185806: contig of 2336 ocation/Qualifiers
1042	/or /dr
2216: contig of 10	/chromosome="UNK"
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139098: gap of unkno)
140570. Anntia of 10	misc feature 113469. 120753

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Gaps

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Indels

Length 91531;

LOCUS AC079846 Accession AC079846

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Fragment Name Begin End AC079846_0 110000 110000 AC079846_2 200001 310000 AC079846_3 300001 391531 Continuation (4 of 4) of AC079846 from base 300001 (AC079846 Homo sapiens chromoson
                                                                                                                                                                                                                                                                                                              Query Match
2.4%; Score 35; DB 2; Le
Best Local Similarity 100.0%; Pred. No. 1.4e-08;
Matches 35; Conservative 0; Mismatches 0;
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383 AAGATCGAGACCCTGCGCTTCGCCCACAACTACAT 417
                                                                                                                                         Sequence split into 4 fragments
                                                                    RESULT 10
AC079846_3/c
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ASPAGSDMDYMOPPPPDKHRYAPHLPTARDCI"
a 1536 c 1507 g 1596 t
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 6123)
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Submitted (06-SEP-2000) Center for Basic Neuroscience - NA4.146,
Southwestern Medical Center, 5323 Harry Hines Boulevard, Dallas,
75390-9111, USA
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Neurogenin2 expression in ventral and dorsal spinal neural
progenitor cells is regulated by distinct enhancers
Dev. Biol. 229 (2), 327-339 (2001)
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                                                                                                                                                                                                                                   Length 185806;
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Homo saplens neurogenin 2 gene, partial cds.
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Best Local Similarity 100.0%; Pred. No. 1.7e-08;
Matches 35; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                Ouery Match 6.3%; Score 92; DB 2; L. Best Local Similarity 100.0%; Pred. No. 1.2e-42; Matches 92; Conservative 0; Mismatches 0;
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162444. .185806
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Db 159187 ATCGAGACCCTGCGCTTCGCCCACAACTACAT 159218
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         120854. .129342
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ACU23886 179697 bp DNA linear PRI 20-MAR-2002
Homo sapiens BAC clone RP11-402J6 from 4, complete sequence.
AC023886
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Submitted (15-MAR-2002) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis, MM 05108, USA
5 (bases 1 to 179697)
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Submitted (20-MAR-2002) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
On Mar 15, 2002 this sequence version replaced gi:17352441.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (18-FEB-2000) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis, MO 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping
                                                                                                                                                                                                                                                                      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Center: Washington University Genome Sequencing Center
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Radionenko,M. and Abbott,A.
The sequence of Homo sapiens BAC clone RP11-402J6
Unpublished (2001)
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Contact: sapiens@watson.wustl.edu
------- Summarv Stafistics
                                                                                                                                                                                                                                                                                                                                                                             Toward a complete human genome sequence Genome Res. 8 (11), 1097-1108 (1998)
DD 86995 AAGATCGAGACCTGCGCTTCGCCCACAACTACAT 86961
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                                                                                                                                                                                                                                                                                                                                   1 (bases 1 to 179697)
Sulston,J.E. and Waterston,R.
                                                                                                                                                                                                   AC023886.7 GI:19482381
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Waterston, R.H.
Direct Submission
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Gaps

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Indels

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819 AAGATCGAGACCCTGCGCTTCGCCCACAACTACAT 853

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clone sections once, or longer because we provide a small overlap between neighboring data submissions.
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This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest

MAPPING INFORMATION:

Mapping information for this clone was provided by Dr. John D. McPherson, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see http://genme.wustl.edu/gsc

SOURCE INFORMATION:

The RPCI-11 human BAC library was made from the blood of one male donor, as described by Osoegawa, K., Woon, P.Y., Zhao, B., Frengen, E. Tateno, M., Catanese, J.J. and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from Research Genetics, Inc. (http://www.resgen.com) or Pleter de Jong and coworkers at http://www.chori.org pBACe3.6 VECTOR:

NEIGHBORING SEQUENCE INFORMATION:

The clone sequenced to the left is AC004049, 2000 bp overlap; the clone sequenced to the right is RP11-148B6. Actual end of this clone is at base postition 179697 of RP11-402J6.

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repeat_region

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repeat_region

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1474. 14795
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72792 . 33487 /rpt_family="Li" 33488 . 33488 7rpt_family="MalR" 33848 . 34554 4358 . 34379 rpt_family="MaLR" . .32791 2461 repeat_region repeat_region repeat_region

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34381...34502 7rpt_fanlly...Alu... 34503...3456 7rpt_fanlly...Ll... 7457...34859 7rpt_fanlly...Alu... 34860...35041 4860. .35041 rpt_family="L1" 35219. .35676 /rpt_fam11y="1 repeat_region repeat_region repeat_region repeat_region

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repeat_region

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AAGAGCGAGTTGGCACTGAGCAAGCAGCGACG
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AF234829
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NCABAEEGCRGAPPKLRARGGRSPPKSELALSKORRSRRKKANDRERNRHIDLNSA
IDALRQVLPTPPDDAKLTKIETLRFAHNYIWALTQTLRIADHSLYALEPPAPHCGELG
SPGAPGWGSLYSPVGSLSPASLEERPGLLGATSSACLSPGSLAFSDFL"
459 c 413 g 228 t
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Submitted (16-MAR-1999) Ravassard P., Lgn, CNRS UMRC 9923, Hopital
de la Pitie Salpetriere, Bat. CERVI, 83 Bd. de l'Hopital, 75013
PARIS, FRANCE
                                                                                                                                                                                                                                                                                                                                                                                                       The human neurogenin 3 homolog maps to chromosome 10q21.3 and its expression pattern is identical to that of its murine counterparts Unpublished
                                                                                                                                                                                                                                                                                                                                                      Euteleostom1;
/rpt_family="Alu"
39941. .40230
/rpt_family="Alu"
39941. .39956
/note="match to EST AA775240 (NID:92834574) ad18a05.s1"
40767. .40798
                                                                                                                                                                                                                                                                                                             3; ngn3 gene
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1330)
Rayassard,P., Icard-Liepkalns,C., Wlard,L., Julien,J.P. and
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                                                                                                                                                                                                                                                 HSA133776 1330 bp DNA Homo sapiens gene for neurogenin 3. AJ133776.1 GI:5123782 BLH transcription factor; neurogenesis;
                                                                                              Query Match 2.4%; Score 35; DB 9; I
Best Local Similarity 100.0%; Pred. No. 1.4e-08;
Matches 35; Conservative 0; Mismatches 0;
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/gene="ngn3"
/function="early neurogenesis"
                                                                                                                                                    2.2%; but
100.0%; Pred. No. 1.00.0%; Mismatches
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/gene="ngn3"
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/db_xref="G1:5123783"
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/gene-"ngn3"
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/gene="ngn3"
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Ravassard, P.
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Best Local Similarity 100.
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/traislation="MTPQPSGAPTVQVTRETERSFPRASEDEVTCPTSAPPSPTRTRG
NCAREABEGGCRAPRKLRARRGGRSPRYSELALSKQRRSRRKANDRSBRNRMHUNSA
LDALRGVLPTPPDDAKLTY LPTLRFHNY IVALTGTLRIADISLYALEPPAPICGELG
SPGGSPGONGSLYSPYGQAGSLSPAALLEBRPGLLGATSSACLSPGSLAFSDFL"
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Human DNA sequence from clone RPI1-34333 on chromosome 10, complete
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del Bosque-Plata,L., Lin,J., Horikawa,Y., Schwarz,P.E., Cox,N.J.,
Iwasaki,N., Ogata,M., Iwamoto,Y., German,M.S. and Bell,G.I.
Mutations in the coding region of the neurogenin 3 gene (NEUROG3)
are not a common cause of maturity-onset diabetes of the young in
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 165110)
Howden, P.
                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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California San Francisco, 513 Parnassus Ave., San Francisco,
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Homo sapiens neurogenin 3 gene, complete cds.
AF.234829
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100.0%; Pred. No. 1e-06;
tive 0; Mismatches (
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/product="neurogenin 3"
/protein_id="AAK15022.1"
/db_xref="GI:13183003"
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/organism="Homo sapiens"
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/product="neurogenin 3"
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Diabetes 50 (3), 694-696 (2001)
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17719. .18069
// note="LiMC4 repeat: matches 7617. .7977 of consensus" 18117. .18345
// note="MIR repeat: matches 7. .262 of consensus" 19169. .19400
// note="MIR repeat: matches 5. .239 of consensus" 19436. .19627
// note="LiMC5 repeat: matches 7728. .7917 of consensus" 19642. .19716
// note="MIR repeat: matches 48. .131 of consensus" 19642. .19716
// note="MIR repeat: matches 48. .131 of consensus" 19642. .19716
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="MLT1F repeat: matches 188. .541 of consensus" 21463. .21618
/note="MIR repeat: matches 46. .192 of consensus" 22019. .22326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="lizergeat: matches 2453. .2629 of consensus" 22896. .23174
//note="Will repeat: matches 117. .413 of consensus" 23215. .23346
//note="Will repeat: matches 48. .188 of consensus" 23388. .23532
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24291. 24581
24291. 24581
24653. 24850
70cte="MIR repeat: matches 1. .200 of consensus" 24653. 24850
70cte="MIR repeat: matches 1. .200 of consensus" 26889. 26885
70cte="MIR repeat: matches 1. .200 of consensus" 70cte="MIR repeat: matches 1. .200 of consensus" 70cte="CpG island"
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Acte-"Alze repeat: matches 29. .275 of consensus" 32767. .32830
Anote-"MIR repeat: matches 76. .139 of consensus"
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                                                                                                                                                                                                                 1881 repeat: matches 2. .114 of consensus. 8069
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                                    .109 of consensus"
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                                                                                                                                  .140 of consensus"
                                                      15404. 15613
/hote-"MIR repeat: matches 3. .213 of consensus"
16626. 16705
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="1" copies 2 mer tg 100% conserved"
20623. 20704
/note="41 copies 2 mer gt 85% conserved"
20738. 20773
/note="02 repeat: matches 1. .36 of consensus"
20802. 20863
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/note="43 copies 3 mer tcc 72% conserved"
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                                 repeat: matches 9.
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17476. 17569
70ote="MER81 repeat: matches 2
17719. 18069
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                                                                                                                                /note-"MIR repeat: matches
16928. .16993
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/note="CpG island"
/evidence=not_experimental
31084. .31156
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/note="CpG island"
/evidence=not_experimental
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/note="MLT1F
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               Juleacu Submission.

Submitted (12-JUL-2001) Sanger Centre, Hinxton, Cambridgeshire, CBIO 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requestes: clonerques/ganger.ac.uk

On Jul 8, 2001 this sequence version replaced gi.14575291.

During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quallity data (i.e., phred quallity) as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with thair source databases: Em: EMBL: Sw:, SWISSPROT; Tr:, TREMBL: Wp:, WORMPEP; Information on the WORMPEP http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromaphing Group. Further information can be found at change of constructed by the Sanger Centre Chromosome 10 Mapping Group. Further information can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   http://www.sanger.ac.uk/HGP/Chhilo
RP11-34333 is from the library RPCI-11.2 constructed by the group
of Pieter de Jong. For further details see
http://www.chori.org/bacpac/home.htm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This sequence is the entire insert of clone RPI1-343J3 The true left end of clone RPI1-242G20 is at 139955 in this sequence. The true right end of clone RPI1-404C6 is at 6588 in this sequence. Location/cualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6916. 8080
/note="LIMEc repeat: matches 1168. 2367 of consensus"
9934. 10087
/note="MIR repeat: matches 25. 184 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   matches 118. .293 of consensus"
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/note="AluSq repeat: matches 243. .299 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="AluSx repeat: matches 1. .134 of consensus"
4319. .4494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="AluSx repeat: matches 1. .294 of consensus"
11600. .11639
//note="30 copies 2 mer tc 95% conserved"
12479. .12608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             note="THE1C repeat: matches 2. .142 of consensus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .194 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               note-"MIR repeat: matches 2. .148 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Further information can be found at
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13433, .13876
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note="MIR repeat: matches 65.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Homo sapiens"
/db_xref="taxon:9606"
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/clone="RP11-343J3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 136. 1187
note="26 copies 2
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                                                                                                           note="Aluex repeat: matches 1. .292 of consensus"
40050. .41189
Anote="Mir repeat: matches 1. .144 of consensus"
41057. .41290
Aluex matches 8. .240 of consensus"
41296. .41460
Aluex matches 1916. .2416 of consensus"
Alsoe. .41944
Anote="L2 repeat: matches 1916. .2416 of consensus"
Alsoe. .41944
Anote="L2 repeat: matches 1916. .2416 of consensus"
Alsoe. .42698
Alsoe. .4459
Anote="LTRIC repeat: matches 1. .371 of consensus"
Anote="LTRIC repeat: matches 1. .371 of consensus"
Alsoe. .4456
Anote="LTRIA repeat: matches 37. .97 of consensus"
Alsoe. .45300
Anote="LTRA1 repeat: matches 90. .192 of consensus"
Anote="LTRA1 repeat: matches 90. .192 of consensus"
Anote="Aluex repeat: matches 1. .287 of consensus"
Anote="Aluex repeat: matches 1. .300 of consensus"
Anote="Aluex repeat: matches 1. .300 of consensus"
Anote="Aluex repeat: matches 1. .300 of consensus"
Anote="Aluex repeat: matches 2. .167 of consensus"
Anote="Aluex repeat: matches 2. .167 of consensus"
Anote="EAM repeat: matches 2. .167 of consensus"
Anote="LIMA repeat: matches 3865. .4055 of consensus"
Anote="LIMA repeat: matches 3652. .3865 of consensus"
Anote
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Anderson,S., Baldwin,J., Barna,N., Beckerly,R., Beda,F.,
Boguslavkty,L., Boukhgalter,B., Brown,A., Burkett,G., Castle,A.,
Choepel,Y., Colangelo,M., Collins,S., Collymore,A., Cooke,P.,
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 173341)
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55237. .55700
                                                                                                    'note-"AluSx repeat: matches 1. .292 of consensus"
                                        .219 of consensus"
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39214. .39423
/note-"MIR repeat: matches 3.
39489. .39801
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HTG; HTGS_PHASE1; HTGS_DRAFT.
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Matches 32; Conserva
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Direct Submission

Direct Submission

Submitted (22-JAN-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA

Research, 320 Charles Street, Cambridge, MA 02141, USA

Biran, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Anderson, S., Balduh, J., Basna, A., Burkett, G., Edga, F., Campoplano, A., Castle, A., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L., Karattas, A., Kerneira, P., Filtzhugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L., Karattas, A., Kerneira, P., Filtzhugh, W., Gardyna, S., Ginde, S., Goyette, M., Graham, L., Karattas, A., Kerneira, F., Lakocque, K., Lakoc, C., Liu, G., Locke, K., Macdonald, P., Marquis, N., McEwan, P., McCher, K., Lakocdue, K., Lakocque, K., Lakocke, K., Macdonald, P., Marquis, N., McEwan, P., McCher, M., McKernan, K., Meheus, L., Mhova, T., Miranda, C., Mlenga, V., Morrow, J., Murphy, T., Naylor, J., Norman, C. H., O'Connor, T., Santos, M., Schlauc, S., Severy, P., Spencer, N., Stantos, M., Stolanovic, N., Subramanian, A., Taraylio, J., Taraylio, J., Taraylio, J., Vasiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zalnoun, J., Zimmer, A. and Zody, M.

All repeats were identified using RepeatMasker:

Smit, A.F., A. Green, P. (1996-1997)

http://ftp.genome.washingtor.edu/RM/RepeatMasker:

Contern Contern Conne.washingtor.edu/RM/RepeatMasker:

Contern Conne. Research
DeArellano, K., Dewar, K., Domino, M., Doyle, M., Fenestor, J., Ferreira, P., FitzHugh, W., Forrest, C., Gage, D., Galagan, J., Gardyna, S., Grant, G., Hagos, W., Heaford, A., Horton, L., Howland, J.C., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., Handers, T., Lehoczky, J., Levine, R., Lieu, C., Liu, G., Locke, K., Macdonald, P., Marquis, N., McEwan, P., McGurk, A., McKernan, K., McPheeters, R., Maldrim, J., Momeus, L., Morrow, J., Naylor, J., Peterson, K., Polerre, R., O'Connor, T., O'Donnell, P., Olivar, T.M., Peterson, K., Peterson, K., Polara, V., Raymod, C., Riley, R., Rothman, D., Roy, A., Santos, R., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Tirrell, A., Vassillev, H., Viel, R., Vo, A., Wu, X., Wyman, D., Ye, W. J., Zimmer, A. and Zody, M.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: sequence_submissions@genome.wi.mit.edu
Contact project Information
Center project Information
Center clone name: 57_E_12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Quality coverage: 3.7 in Q20 bases; agarose-fp Quality coverage: 3.8 in Q20 bases; sum-of-contigs
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Insert size: 171041; sum-of-contigs
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misc_feature

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18891 128990: gap of 100 bp
18991 147290: contig of 18300 bp in length
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                                                                        74: gap of 100 bp in length 1881: contig of 5057 bp in length 23526: contig of 100 bp
                                                                                                                                                                                                                                     2673 38632: contig of 5960 bp in length 8633 38732: gap of 100 bp 8733 43735: contig of 5003 bp in length
                                                                                                                                                                                                                                                                                                                 49120: gap of 100 bp
53660: contig of 4540 bp in length
53760: gap of 100 bp
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 100 bp
f 2746 bp in length
                               of 100 bp
contig of 2990 bp in length
                                                              9: gap of 100 bp
13674: contig of 4595 bp in length
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49020: contig of 5185 bp in length
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clone_lib-"RPCI-11 Human Male BAC"
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2673 38632: con
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 3: gap of
5889: con
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8979: con
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Best Local Similarity 100.0%; Pred. No. 8.6e-07;
Matches 32; Conservative 0; Mismatches 0;
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Search completed: April 8, 2003, 20:41:55 Job time : 5789 secs

Chicken atonal hom DNA encoding murin Mouse neurogenic d

PCR primer used to Mouse neurogenin 1

Murine neurogenin

Human cDNA encodin Neurogenin-3 Mouse atonal homol Mouse atonal homol Human neurogenic d DNA encoding human Human neurogenic d DNA encoding human Human NeuroD2 gene

Mouse neurogenin 2

Murine neurogenin Mouse neurogenin

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Basic helix-loop-helix; BHLH; RELAX; Rat Embryonic Longitudinal Axis; control; gene expression; transcriptional activator; targeting; protein expression; central nervous system; CNS; treatment; nervous system disorder; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cDNA encoding a novel BHLH protein designated RELAX.
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/product= RELAX
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Rat spliced transc
Mouse spliced tran
Human neurogenin 3
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Murine neurogenin-
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8791.223 Million cell updates/sec
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| SIDS2/gcgdata/geneseqn-embl/Nal982.DAT:*
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                 GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Notal number of hits satisfying chosen parameters:
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Score

Result Ş. 7225555 72255555 73255555

Oligonucleotide fo Oligonucleotide fo Acetylcholine tran NACHR beta2 subuni

Human reproductive Human reproductive 1mmune/haema Human 1mmune/haema

Scoring table:

Word size :

Searched:

Database :

Perfect score:

Sequence:

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M. capsulatus gene M. capsulatus gene M. capsulatus gene

Arabidopsis thalia Arabidopsis thalia

Human reproductive Human testicular a

Human reproductive Human testicular a

Human immune/haema

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             CCAACGACCGGGAGCGCAACCGCATGCACAACCTTAACTCCGCGCTGGATGCGCTGCGCG
                                                                        GTGTCCTGCCCACCTTCCCGGATGACGCCAAACTTACAAAGATCGAGACCCTGCGCTTCG
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160..804
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                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                         The present sequence encodes a basic helix-loop-helix (BHLH) type protein, designated RELAX (Rat Embryonic Longitudinal Axis) protein. The protein is used to control and participate in gene expression, by acting as transcriptional activator, strictly dependent on the presence of an intact E box (CANNTG), particularly for targeting expression of proteins to the central nervous system (CANNTG). The nucleic acid sequence can be used to treat nervous system disorders, and antisense sequences can be used to control mRNA transcription.
                                                                                                                                                                                                                                                                                                                                                                                     1 GCAGGTAGCGAGAGGAGCAGTCCCTGGGCCCCCGTTGCTGATTGGCCCGTGGCACAGGCA 60
                                                                                                                                                                                                                                                                                                                                                                                                       CGCCCACCATCCCAAGTGTCCCCAAGAGACCCAGCAACCCTTTCCCGGGAGCCTCGGACCACG
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                                                                                                                                                                                                                                                                                                                            DB 19; Length 1491;
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                                                                         ٤, ٦
                                                                     Basic helix-loop-helix polypeptide and related nucleic acid
transcriptional activity, for targeting expression of genes
central nervous system and treatment of nervous disease
                                                                                                                                                                                                                                                                                                                                                           0; Indels
                                                                                                                                                                                                                                                                                                Sequence 1491 BP; 307 A; 487 C; 413 G; 284 T; 0 other;
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                                                                                                                                                                                                                                                                                                                          100.0%; Score 1460;
100.0%; Pred. No. 0;
iive 0; Mismatches
 Icard-Liepkalns
                                                                                                                                 Claim 6; Page 20; 28pp; French.
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                           WPI; 1998-362775/31.
P-PSDB; AAW62991.
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The patent discloses a method for inducing non-neuronal cells (NNC) to differentiate into neurons and for NNCs to express a neuronal subtype-special marker. Transformed host cells are used as sources of neuronal and other growth factors; in culture for screening compounds that modulate neural differentiation or as sources of recombinantly produced neurogenins and Phox2a proteins for use in transplantation. The cells also have a variety of in vivo uses, e.g. for transplantation at sites of neuronal dysfunction e.g. patients with hearing or vision loss due to optical or auditory nerve damage, brain or spinal cord injuries, and neurodegenerative disorders e.g. Alzheimer's disease. The present sequence encodes mutine neurogenin-3 (NGN-3), a transcription factor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     transcription factor that induces a core program of neurogenesis. Forced expression of murine NOSI can elicit expression of at least some neuronal phenotypic markers even in NNCs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Atonal; homologue; orthologue; atonal-associated protein; deafness; hearing impairment; vestibular effect; balance disorder; osteoarthritis; cellular proliferation; cerebellar granule neuron; gene therapy; mechanoreceptive cell growth; auditory; osteopathic; cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NNCs differentiate into neurons through the recombinant expression of
                                                                                                                                                                                                                               Inducing non-neuronal cells to differentiate into neurons and for non-neuronal cells to express a neuronal subtype-specific marker, comprising contacting the non-neuronal cells with a vector containing neurogenin nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 762 GCGCTGGATGCGCTGCCGGTGTCCTGCCCACCTTCCCGGATGACGCCAAACTTACAAAG 821
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Pred. No. 9.3e-35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mouse neurogenin 3 (ngn3) cDNA, SEQ ID NO:24.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Pred. no.
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                                                                                                                                                                                                                                                                                                                                             Claim 1; Fig 1J; 76pp; English.
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99WO-US18525
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Matches 92; Conservative
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P-PSDB; AAY70570.
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                                                                                                                               Anderson DJ,
13-AUG-1999;
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                                          14-AUG-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The Mouse neurogenin 3 is one of several neurogenin proteins discussed in the present invention. The neurogenin nucleic acids can be expressed in a host cell, transformed using an expression vector, to produce recombinant proteins. The proteins and the antibodies raised against the proteins are useful in the study of neurogenesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GCGCTGGATGCGCTGCGCGGTGTCCTGCCCACCTTCCCGGATGACGCCAAACTTACAAAG 821
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                            Mouse neurogenins, useful in neurogenesis – and recombinant nucleic acids and proteins derived from rat and Xenopus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 6.3%; Score 92; DB 19; Length 804; Best Local Similarity 100.0%; Pred. No. 9.3e-35; Matches 92; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Neurogenin-3; NGN-3; non-neuronal cell; NNC; neurogenesis;
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/product= "Murine neurogenin-3 protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 804 BP; 171 A; 263 C; 225 G; 145 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Murine neurogenin-3 (NGN3) nucleic acid sequence.
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160..804
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96US-0722570.
96US-0030864.
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                                                                                                             97WO-US17048
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27-SEP-1996;
12-NOV-1996;
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The human neurogenin 3 Ngn3 DNA sequence AAC61089 encodes the Ngn3 protein AAX88517. The Ngn3 gene is located at chromosome position 10922.1-22.2. The invention relates to the human Ngn3 nucleotide and protein sequences, and includes an antibody recognising the Ngn3 protein. Also included in the invention is a method for identifying an islet cell precursor, the method involves analysing a cell for the expression of the Ngn3 gene product, where detection of the product is indicative of an islet cell precursor. The Ngn3 DNA sequence is useful as a diagnostic reagent for detecting (in a subject) a predisposition to a defect in Ngn3 activity. The Ngn3 protein is useful for identifying beta-cell precursor cells expression Ngn3 activity. The Ngn3 protein is useful for identifying beta-cell precursor cells expression beta-cells to treat patients with diabetes mellitus. The present sequence represents the murine Ngn3 genomic DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Atonal; homologue; orthologue; atonal-associated protein; deafness; hearing impairment; vestibular effect; balance disorder; osteoarthritis; callular proliferation; cerebellar granule neuron; gene therapy; mechanoreceptive cell growth; auditory; osteopathic; cytostatic; transgenic animal; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1396 GCGCTGGATGCGCTGCGCGGTGTCCTCCCCGGATGACGCCAAACTTACAAAG 1455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            762 GCGCTGGATGCGCTGCGCGGTGTCCTGCCCACCTTCCCGGATGACGCCAAACTTACAAAG 821
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                          Novel human neurogenin 3 polypeptides and polynucleotides encoding them, useful for diagnosis, prevention and treatment of diabetes mellitus and to identify individuals at risk of diabetes -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 1861;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mouse atonal homologue 5 (ATOH5, Math4B) cDNA, SEQ ID NO:4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1861 BP; 397 A; 560 C; 537 G; 367 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Match 6.3%; Score 92; DB 21; Local Similarity 100.0%; Pred. No. 9e-35; es 92; Conservative 0; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1456 ATCGAGACCCTGCGCTTCGCCCACAACTACAT 1487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       822 ATCGAGACCCTGCGCTTCGCCCACAACTACAT 853
                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 18; Page 49-50; 54pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAF27254 standard; cDNA; 5567 BP.
                                                                                                                                        99US-0128180.
                                                                                          28-MAR-2000; 2000WO-US08436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                              (REGC ) UNIV CALIFORNIA
                                                                                                                                                                                                                                                                           WPI; 2000-664989/64.
                                                                                                                                                                                                                                German MS, Lin J;
                                                                                                                                                                                                                                                                                                   P-PSDB; AAY85618.
  WO200059936-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200073764-A2.
                                                                                                                                        06-APR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24-APR-2001
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                                             12-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sednence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAF27254;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
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                                                                                                                                                                                                                                                                                                                                                                                     amino acid sequence, or any of its homologues or orthologues as therapeutic agents for the treatment of deafness, partial hearing loss, vestibular effects due to damage or loss of inner hair cells, osteoarthritis and abnormal cell proliferation. The invention also encompasses methods of screening for compounds which affect the expression of an atonal-associated nucleic acid sequence, in an animal, and a transgent animal in which an allele of a native atonal-associated inactivating the atonal-associated allele. The nucleic acid sequence, thus may be used in a method of treating an animal for hearing impairment, joint disease, balance disorders, abnormal cell proliferation, or other disease, to loss of a functional atonal-associated nucleic acid or protein. They may particularly be used to treat an animal with a deficiency in cerebellar granule neurons or their precursors, and may
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 also be used in promoting mechanoreceptive cell growth and generating that cells. The present sequence represents an atomal-associated nucleic acid sequence referred to in the invention.

Note: The present sequence is not shown in the specification, but
                                                                                                                                                                                                                            Therapeutic use of atonal-associated nucleic acids or amino acids, or any of its homologs or orthologs, for the treatment of e.g. deafness, osteoarthritis and abnormal cell proliferation -
                                                                                                                                                                                                                                                                                                                                                                    invention relates to the use of atomal-associated nucleic acid or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       463 GCGCTGGATGCGCTGCGCGGTGTCCTGCCCACCTTCCCGGATGACGCCAAACTTACAAAG 522
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               762 GCGCTGGATGCGCTGCGCGGTGTCCTGCCCACCTTCCCGGATGACGCCAAACTTACAAAG 821
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Neurogenin 3; Ngn3; cellular differentiation; diabetes mellitus; islet cell precursor identification; mouse; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
0
                                                                                                                  Ben-Arie N;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 861;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 861 BP; 182 A; 274 C; 250 G; 155 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               f.3%; Score 92; DB 22; L
Local Similarity 100.0%; Pred. No. 9.3e-35;
Nes 92; Conservative 0; Mismatches 0;
                                                                                                                Hassan B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Murine neurogenin 3 (Ngn3) genomic DNA sequence,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       822 ATCGAGACCCTGCGCTTCGCCCACACTACAT 853
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               523 ATCGAGACCCTGCGCTTCGCCCACAACTACAT 554
                                                                                                                Birmingham N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "Neurogenin 3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                    Disclosure; Page -; 142pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /product- "Ngn3"
                                                                     (BAYU ) BAYLOR COLLEGE MEDICINE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAC61090 standard; DNA; 1861 BP.
01-JUN-1999; 99US-0137060.
19-JAN-2000; 2000US-0176993.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           was obtained from GenBank.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              05-FEB-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /*tag= a
                                                                                                              Bellen H,
                                                                                                                                                         WPI; 2001-032190/04.
P-PSDB; AAB60359.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus
                                                                                                              Zoghbi HY,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
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Faigler S;

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messenger RNAs that populate a (sub-)transcriptome, where the ranscriptome comprises messenger RNAs transcriptome comprises messenger RNAs transcriptome from multiple transcription units that populate a genome. The library comprises several oligonuclectides, each capable of hybridising selectively to a set of messenger RNAs transcribed from a given transcription unit of the genome, which encodes one or more messenger RNA splice variants. The oligonuclectide libraries are useful for detecting mRNAs from a biological sample, in expression profilling studies, in qualitatively or quantitatively characterising the corresponding transcriptome, and in detecting RNA transcripts and splice variants of human or animal transcriptomes. The libraries may also be used as specialised minimaries to detect transcripts of a sub-transcriptome under a libraries to detect transcripts of a sub-transcriptome under a capicalised minimaries to detect transcripts of a sub-transcriptome of tissue- and pathology specific genes such as those genes condition; to detect developmental specific genes such as those genes condition; to detect developmental specific genes; and to detect RNA transcripts and splice variants of a transcriptome of a patient suffering from a particular disorder. ABN27253 to ABNS9589 represent
                                                                                                                                                                                                                                                                                                                               New oligonucleotide libraries comprising oligonucleotides which selectively hybridize to mRNAs transcribed from a transcription unit of a genome, useful for detecting tissue-, pathology-, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               the exemplification of the present invention.

N.B. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention describes oligonucleotide libraries for detecting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1252 TTCCTTGCTGCTGTGCGTGCACAAGGACATTGCAGGCTGATCTCCTCTTAACCCTCCTC 1311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 ITCCTTGCTGCTGTGCGGGCGCACAAAGGACATTGCAGGCTGATCTCCTCTTAACCCTCCTC 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mouse spliced transcript detection oligonucleotide SEQ ID NO:30269.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; mouse; rat; splice transcript; detection; RNA transcript; splice variant; transcriptome; oligonucleotide library; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 65; DB 24; Length 65;
Pred. No. 1.8e-21;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 65 BP; 11 A; 20 C; 14 G; 20 T; 0 other;
                                                                                                                                                                                                                       Mintz E, Mintz L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 1; SEQ ID 4140; 47pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity 100.0%; Price 65; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABN57521 standard; DNA; 65 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                       developmental-specific genes
                                                                              28-JUL-2000; 2000US-221607P. 02-MAY-2001; 2001US-287724P.
                       20-JUL-2001; 2001WO-IB01903.
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                                                                                                                                                                                                                       Wasserman A,
                                                                                                                                                                  (COMP-) COMPUGEN INC.
                                                                                                                                                                                                                                                                              WPI; 2002-257383/30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1312 AGTGT 1316
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                                                                                                                                                                                                                       Shoshan A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABN57521;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61
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So acid sequence referred to in the invention.

Note: The present sequence is not shown in the specification, but
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                                                                                                                                                                                                                                                                                                                                                            Therapeutic use of atonal-associated nucleic acids or amino acids, or any of its homologs or orthologs, for the treatment of e.g. deafness, osteoarthritis and abnormal cell proliferation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            762 GCGCTGGATGCGCTGCGCGGTGTCCTGCCCACCTTCCCGGATGACGCCAAACTTACAAAG 821
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to the use of atonal-associated nucleic acid or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 5567;
                                                                                                                                                                                                                          Ben-Arie N;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 5567 BP; 1271 A; 1549 C; 1564 G; 1183 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6.3%; Score 92; DB 22; Length 55(
100.0%; Pred. No. 8.5e-35;
.ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                          Hassan B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5286 ATCGAGACCCTGCGCTTCGCCCACAACTACAT 5317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       822 ATCGAGACCCTGCGCTTCGCCCACAACTACAT 853
                                                                                                                                                                                                                       Birmingham N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Page -; 142pp; English.
                                                                                                                                                               (BAYU ) BAYLOR COLLEGE MEDICINE.
                       01-JUN-2000; 2000WO-US15410.
                                                                              99US-0137060
                                                                                                     19-JAN-2000; 2000US-0176993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 100./
Matches 92, Conservative
                                                                                                                                                                                                                       Coghbi HY, Bellen H,
                                                                                                                                                                                                                                                                           WPI; 2001-032190/04.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rattus norvegicus
                                                                                                                                                                                                                                                                                                        P-PSDB; AAB60350
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                                                                              01-JUN-1999;
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Gaps

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07-FEB-2002

ABN31392;

RESULT 7 ABN31392

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07-FEB-2002.

Shoshan A,

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The human neurogenin 3 Ngn3 DNA sequence AAC61089 encodes the Ngn3 protein AAY85617. The Ngn3 gene is located at chromosome position 10q22.1-22.2. The invention relates to the human Ngn3 nuclectide and Protein sequences, and includes an antibody recognising the Ngn3 protein. Also included in the invention is a method for identifying an islet cell precursor, the method involves analysing a cell for the expression of the Ngn3 gene product, where detection of the product is indicative of an islet cell precursor. The Ngn3 DNA sequence is useful as a diagnostic reagent for detecting (in a subject) a predisposition to a defect in pancreatic islet cell function or formation associated with a defect in precursor cells unction or formation associated with a defect in precursor cells expressing Ngn3, and to alter cellular differentiation in culture in vivo to produce new beta-cells to treat patients with diabetes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; foetal tissue antigen; ss; antiinflammatory; neuroprotective;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    immunomodulator; cardiovascular; cytostatic; nephrothropic; cardiovascular; autoimmune disease; rheumatoid arthritis; hyperproliferative disorder; breast neoplasm; cancer; cardiovascular disorder; cardiac arrest; cerebrovascular disorder; cardiac arrest; cerebrovascular disorder; cardiac arrest; nervous system disorder; Alzheimer's disease; infection; coular disorder; corneal infection; wound healing; epithelial cell proliferation; food additive.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel human neurogenin 3 polypeptides and polynucleotides encodin
them, useful for diagnosis, prevention and treatment of diabetes
mellitus and to identify individuals at risk of diabetes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 5340 BP; 1215 A; 1500 C; 1514 G; 1111 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human cDNA encoding a novel foetal antigen, SEQ ID No 321.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 21; Le 2.1e-05; hes 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3235 AAGAGGAGTTGGCACTGAGCAAGCAGCGACG 3266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           672 AAGAGCGAGTTGGCACTGAGCAAGCAGCGACG 703
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2.2%; Score 32;
                                                                                                                               /note- "Neurogenin 3"
                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 6; Page 46-48; 54pp; English
                                               3022, 3666
/*tag= a
/product= "Ngn3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAS33797 standard; cDNA; 428 BP.
                                                                                                                                                                                                                                                                                       28-MAR-2000; 2000WO-US08436.
                                                                                                                                                                                                                                                                                                                                            99US-0128180
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Best Local Similarity 100.00
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                                                                                                                                                                                                                                                                                                                                                                                             (REGC ) UNIV CALIFORNIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2000-664989/64.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     German MS, Lin J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               P-PSDB; AAY85617
                                                                                                                                                                                   WO200059936-A1.
                                                                                                                                                                                                                                                                                                                                      06-APR-1999;
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                           Key
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The present invention describes oligonucleotide libraries for detecting messenger RNAs that populate a.(sub-)transcriptome comprises messenger RNAs transcribted from multiple transcription units that populate a genome. The library comprises c several oligonucleotides, each capable of hybridising selectively to a several oligonucleotides, each capable of hybridising selectively to a several oligonucleotide libraries are useful for detecting mRNAs from a CC the genome, which encodes one or more messenger RNA splice variants. The oligonucleotide libraries are useful for detecting mRNAs from a blological sample, in expression profiling studies, in qualitatively or quantitatively characterising the corresponding transcriptom, and in c detecting RNA transcripts and splice variants of human or animal transcripts may also be used as specialised minic claranscripts of a sub-transcriptome under a particular biological or pathological state, and so allowing the corresponding transcription of tissue and pathology-specific genes such as those genes only expressed in specific tissue under a specific pathological condition; to detect developmental specific genes; and to detect RNA transcripts and splice variants of a transcriptome of a pattient suffering from a particular disorder. ABN27253 to ABN59589 represent of lignance of the present invention. Of the exemplification of the present invention.

Che exemplification of the present invention. Form part of the printed of the rinted in electronic format directly from WIPO at the rinted of the present processed in specific pathology as pecific pathology.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ó
                                                                                                                                                                                                                                                                                                                                                                                                                    New oligonucleotide libraries comprising oligonucleotides which selectively hybridize to mRNAs transcribed from a transcription unit of a genome, useful for detecting tissue-, pathology-, and developmental-specific genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Neurogenin 3; Ngn3; chromosome 10q22.1-22.2; cellular differentiation; islet cell precursor identification; diabetes mellitus; human; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Indels
                                                                                                                                                                                                                                                                                                                Mintz L, Faigler
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2.4%; Score 35; DB 24; Idarity 100.0%; Pred. No. 8.8e-07; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 65 BP; 16 A; 25 C; 11 G; 13 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human neurogenin 3 (Ngn3) genomic DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             547 TCAGTTCCAAT#CCACCCCACCTAGCCCCACTCTC 581
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 TCAGTTCCAATTCCACCCCACCTAGCCCCACTCTC 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 1; SEQ ID 30269; 47pp; English.
                                                                                                                                                                                                                                                                                                                   Wasserman A, Mintz E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAC61089 standard; DNA; 5340 BP
                                                                                                                               20-JUL-2001; 2001WO-IB01903
                                                                                                                                                                                 28-JUL-2000; 2000US-221607P
                                                                                                                                                                                                          02-MAY-2001; 2001US-287724P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                              (COMP-) COMPUGEN INC.
                                                                                                                                                                                                                                                                                                                                                                     WPI; 2002-257383/30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
es 35; Conserv
                   WO200210449-A2.
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Gaps

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05-FEB-2001

AAC61089;

RESULT 9

Query Match

Matches

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Length 5340;

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2000US-0241785.
2000US-0241786.
2000US-0241787.
2000US-0241808.
2000US-0241826.
2000US-0241826.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                           -NOV-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2000US-0234998
2000US-0235484
                                                                                      2001WO-US01321
                            WO200155312-A2
                                                                                                                 31-JAN-2000; 2

04-FEB-2000; 2

24-AFR-2000; 2

16-MAR-2000; 2

17-MAR-2000; 2

17-MAR-2000; 2

17-MAR-2000; 2

19-MAR-2000; 2

19-MAR-2000; 2

19-MAR-2000; 2

19-JUL-2000; 2

11-JUL-2000; 2

11-JUL-2000; 2

26-JUL-2000; 2
Homo sapiens.
                                                                                     17-JAN-2001;
                                                          02-AUG-2001
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antigens. The nucleic acids and proteins are used to prevent, treat (e.g. rabbits, goats, horses, cats, dogs, chickens or sheep. They are also used in diagnosing a pathological condition in e.g. humans, mice, are also used in diagnosing a pathological condition or susceptibility to a pathological condition. The antibodies to the antigens can also be used in alleviating symptoms associated with the disorders and in diagnostic immunosasays e.g. radioimmunosasays or enzyme linked immunosorbent assays (ELISA). Disorders which are diagnosed or treated immunosorbent assays (ELISA). Disorders which are diagnosed or treated include autoimmuno diseases e.g. rheumatoid arthrilis, carboroliferative disorders e.g. cardiac arrest, cerebrovascular disorders e.g. cardiac arrest, cerebrovascular disorders e.g. cardiac arrest, verebrovascular disorders e.g. cardiac arrest, verebrovascular disorders e.g. corneal infection. The polypeptides can also be used to aid wound healing and epithelial cell proliferation, to
                                                                                                                                                                                                                                                                                                                                                       The invention relates to novel nucleic acids encoding novel human foetal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       prevent skin aging due to sunburn, to maintain organs before transplantation, for supporting cell culture of primary tissues, to regenerate tissues and in chemotaxis. The polypeptides can also be use a food additive or preservative to increase or decrease storage capabilities, fat content, lipid, protein, carbohydrate, vitamins, minerals, cofactors and other nutritional components. Numerous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     examples of diseases and disorders treated by the nucleic acids and proteins are given in the specification. The present sequence
                                                                                                                                                             New polynucleotides and polypeptides for diagnosing, treating, preventing or prognosing e.g. diseases or disorders of the nervous, musculoskeletal, excretory, gastrointestinal, reproductive, and
                                                                                                                                                                                                                                                                                                 SEQ ID No 321; 642pp; English.
                            Ruben SM;
                      Rosen CA, Barash SC,
                                                                              2001-488782/53.
                                                                                                                                                                                                                                               respiratory systems
                                                                                                          P-PSDB; AAU20977
                                                                                                                                                                                                                                                                                               Claim 1;
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                      Gaps
                      0
       Length 428;
Score 29; DB 22; Length ....
Pred. No. 0.0007;
  2.0%; Scc.
100.0%; Pre-
                      Conservative
              Similarity
        Ma.
Local S...
29;
       Query Match
                     Matches
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RESULT 11

ABT03700/c ID ABT03700 standard; DNA; 26 BP.

ABT03700;

13-SEP-2002 (first entry)

Human Neurogenin-3 gene PCR primer SEQ ID NO: 221.

cancer; neoplastic disease; tumour specific marker; cytostatic; transcription factor; PCR; primer; ss. Human;

Homo sapiens

W0200240716-A2.

23-MAY-2002

13-NOV-2001; 2001WO-US43461.

16-NOV-2000; 2000US-249508P.

Palm K;

(CEMI-) CEMINES LLC. PX A X B X B X B X S X X X X X B X X B X X B X X B X X B X X B X X B X X B X X B X

The present invention relates to a method for determining the presence of neoplastic molecular markers in a host, involving the use of neoplastic molecular marker specific reagents to detect such markers and analysing the array of reagents, allowing the identification of the neoplastic Determining the presence of neoplastic molecular markers, by identifying the presence of markers in host test sample using array of neoplastic molecular marker specific reagents and analyzing the array disease present. This can be used to determine the best treatment or cancers, in particular neural cell, lung and prostate tumours. The present sequence is a PCR primer useful for detecting the coding sequences of markers of the invention. Length 26; 0; Indels Score 26; DB 24; Pred. No. 0.024; Sequence 26 BP; 3 A; 10 C; 5 G; 8 T; 0 other; 1.8%; bcc. 100.0%; Pred. No. c. '. 0; Mismatches 673 AGAGCGAGTTGGCACTGAGCAGCAG 698 Example 1; Page 17; 41pp; English. AGAGCGAGTTGGCACTGAGCAAGCAG 1 Query Match 1.8 Best Local Similarity 100. Matches 26; Conservative WPI; 2002-537346/57. the reagents 56 QQ ò

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of

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Gaps

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(first entry) 05-0CT-1998 AAV42515;

AAV42515 standard; DNA; 25 BP

RESULT 12 AAV42515

PCR primer used to isolate part of the RELAX protein coding region.

Basic helix-loop-helix; BHLH; RELAX; Rat Embryonic Longitudinal Axis; control; gene expression; transcriptional activator; targeting; protein expression; central nervous system; CNS; treatment; nervous system disorder; CIG235; PCR primer; ss.

Rattus sp. Synthetic

WO9827206-A2

25-JUN-1998

19-DEC-1997;

(RHON) RHONE-POULENC RORER SA

96FR-0015651.

19-DEC-1996;

Mallet J, Ravassard P, Icard-Liepkalns C;

WPI; 1998-362775/31.

- with Basic helix-loop-helix polypeptide and related nucleic acid transcriptional activity, for targeting expression of genes central nervous system and treatment of nervous disease

Example 2; Page 12; 28pp; French.

a basic helix-loop-helix (BHLH) type protein, designated RELAX (Rat Embryonic Longitudinal Axis) protein. The PCR product is termed CIG235. The protein is used to control and participate in gene expression, by acting 4s transcriptional activator, strictly dependent on the PCR primers AAV42515-16 are used to isolate part of the DNA encoding

Neurogenin-1; NGN-1; non-neuronal cell; NNC; neurogenesis; Phox2a protein; neuronal subtype-specific marker; growth factor; neuronal differentiation; transplantation; neuronal dysfunction; optical nerve damage; auditory nerve damage, neurodegenerative disorder; neuroprotective; nootropic; anticonvulsant; antiparkinsonian; vulnerary; cerebroprotective; immunesuppressant; antilnfectious; ss.

Murine neurogenin-1 (NGN1) nucleic acid sequence.

(first entry)

04-JUL-2000

AAZ51977;

/product= "Murine neurogenin-1 protein"

Location/Qualifiers

Mus sp

Key

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/*tag=

WO200009676-A2

304 GAGCGCAACCGCATGCACAACCT 326

BP.

AAZ51977 standard; DNA; 738

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RESULT 14
AA251977
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The mouse neurogenin 1 is one of several neurogenin proteins discussed in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 the present invention. The neurogenin nucleic acids can be expressed in a host cell, transformed using an expression vector, to produce recombinant proteins. The proteins and the antibodies raised against the proteins are useful in the study of neurogenesis.
                                                                                Gaps
presence of an intact E box (CANNTG), particularly for targeting expression of proteins to the central nervous system (CNS). The nucleic acid sequence can be used to treat nervous system disorders, and antisense sequences can be used to control mRNA transcription.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mouse neurogenin's, useful in neurogenesis - and recombinant nucleic acids and proteins derived from rat and Xenopus
                                                                               ö
                                                                                                                                                                                                                                    ss; Mouse; neurogenin; expression vector; recombinant protein; antibody; neurogenesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                llarity 100.0%; Pred. No. 0.59; Conservative 0; Mismatches 0; Indels
                                                    Score 25; DB 19; Length 25; Pred. No. 0.073;
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                                                                                                                                                                                                                                                                                                    /*tag= a //product= "Mouse neurogenin 1"
                                            Sequence 25 BP; 5 A; 9 C; 6 G; 5 T; 0 other;
                                                                     Local Similarity 100.0%; Pred. No. 0.0 es 25; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                               (CALY ) CALIFORNIA INST OF TECHNOLOGY
                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                 750 AACCITAACTCCGCGCTGGATGCGC 774
                                                                                                          1 AACCTTAACTCCGCGCTGGATGCGC 25
                                                                                                                                                                BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 5; Fig 4; 106pp; English,
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sommer L;
                                                                                                                                                                                                                                                                                                                                                                                 97US-0932411.
96US-0722570.
96US-0030864.
96US-0772009.
                                                                                                                                                               AAV27046 standard; cDNA; 738
                                                                                                                                                                                                                                                                                                                                                                 97WO-US17048
                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                     Mouse neurogenin 1 gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1998-230702/20.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 23; Conserv
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                                                                                                                                                                                                                                                                                                             Anderson DJ,
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19-DEC-1996;
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(CALY) CALIFORNIA INST OF TECHNOLOGY.

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Anderson DJ,

WPI; 2000-256250/22. P-PSDB; AAY70566.

99WO-US18525. 98US-0096630.

13-AUG-1999; 14-AUG-1998;

24-FEB-2000

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The patent discloses a method for inducing non-neuronal cells (NNC) to differentiate into neurons and for NNCs to express a neuronal subtype specific marker. Transformed host cells are used as sources of neuronal and other growth factors; in culture for screening compounds that meurogenins and Phox2a proteins for use in transplantation. The cells also have a variety of in vivo uses, e.g. for transplantation at sites of neuronal dysfunction e.g. patients with hearing or vision loss due to optical or auditory nerve damage, brain or spinal cord injuries, and neurodeencreinve disorders e.g. Alzheimer's disease. The present sequence encodes muxine neurogenin-1 (NGN-1), a transcription factor. NNCs differentiate into neurons through the recombinant expression of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              transcription factor that induces a core program of neurogenesis. Forced expression of murine NGNI can elicit expression of at least some neuronal phenotypic markers even in NNCs. This can be used in autografting.
Inducing non-neuronal cells to differentiate into neurons and for non-neuronal cells to express a neuronal subtype-specific marker, comprising contacting the non-neuronal cells with a vector containing neurogenin nucleic acid -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1.6%; Score 23; DB 21; Length 738; 00.0%; Pred. No. 0.59; ve 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 738 BP; 121 A; 283 C; 205 G; 129 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GAGCGCAACCGCATGCACAACCT 754
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity 100.0%; Pr
                                                                                                                                                                                              claim 1; Fig 1C; 76pp; English.
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Gaps

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732 GAGCGCAACCGCATGCACAACCT 754

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Matches

304 GAGGGCAACCGCATGCACAACCT 326

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AAF27264 standard; cDNA; 790 BP 24-APR-2001 (first entry) AAF27264; RESULT 15

Chicken atonal homologue ngn2/ath4a cDNA, SEQ ID NO:20.

Atonal; homologue; orthologue; atonal-associated protein; deafness; hearing impairment; vestibular effect; balance disorder; osteoarthritis; cellular proliferation; cerebellar granule neuron; gene therapy; mechanoreceptive cell growth; auditory; osteopathic; cytostatic; transgenic animal; ss

Gallus gallus

WO200073764-A2, 07-DEC-2000. 01-JUN-2000; 2000WO-US15410.

01-JUN-1999; 99US-0137060. 19-JAN-2000; 2000US-0176993.

(BAYU) BAYLOR COLLEGE MEDICINE.

Ben-Arie N; Birmingham N, Hassan B, Bellen H, zoghbi HY,

WPI; 2001-032190/04. P-PSDB; AAB60357 Therapeutic use of atonal-associated nucleic acids or amino acids, or any of its homologs or orthologs, for the treatment of e.g. deafness, osteoarthritis and abnormal cell proliferation

Disclosure; Page -; 142pp; English.

and a cid sequence, or any of its homologues or orthologues as therapeutic agents for the treatment of deafness, partial hearing loss, vestibular effects due to damage or loss of inner hair cells, osteoarthritis and abnormal cell proliferation. The invention also encompasses methods of screening for compounds which affect the expression of an atonal-associated nucleic cald sequence in an animal, and a transgenic animal in which an allele of a native atonal-associated nucleic acid sequence, thus of the atonal-associated allele. The nucleic acids or proteins may be used in a method of treating an animal for hearing impairment, joint disease, balance disorders, abnormal cell proliferation, or other joint disease, balance disorders, abnormal cell proliferation, or other classase related to loss of a functional atonal-associated nucleic acid or protein. They may particularly be used to treat an animal with a deficiency in cerebellar granule neurons or their precursors, and may also be used in promoting mechanoreceptive cell growth and generating hair cells. The present sequence represents an atonal-associated nucleic acid or the present sequence represents an atonal-associated nucleic acid sequence referred to in the invention. The invention relates to the use of atonal-associated nucleic acid or was obtained from GenBank

Sequence 790 BP; 91 A; 351 C; 283 G; 65 T; 0 other;

Gaps ; 0 Score 23; DB 22; Length 790; Pred. No. 0.59; 0; Indels Mismatches ; Query Match
1.6%; 8
Best Local Similarity 100.0%;
Matches 23; Conservative 0;

732 GAGCGCAACCGCATGCACAACCT 754

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374 GAGCGCAACCGCATGCACAACCT 396 g

8, 2003, 19:05:41 Search completed: April Job time: 407 secs

OM nucleic

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Searched:

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Sequence 6887, Ap Sequence 11149, A Sequence 12149, A P Sequence 12149, A P Sequence 11, App Sequence 5374, App Sequence 332, App Sequence 332, App Sequence 5673, App Sequence 117, App Sequence 147, App Sequence 147, App Sequence 175, App Sequence 175, App Sequence 18, App Sequence 208, App Sequence 2159, App 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1334, Ap
Sequence 137, App
0 05-09-960-352-14228

0 03-09-960-322-6887

0 03-09-960-322-6887

0 03-09-960-323-1094

0 03-09-864-761-1374

0 03-09-864-761-11

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    756
1074
       April 8, 2003, 17:56:31; Search time 165 Seconds (without alignments) 7761.606 Million cell updates/sec
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1460
1 gcaggtagcgagaggagcag.....agagtgacctaatccagtgt 1460
                        GenCore version 5.1.4\_p5\_4578 Copyright 4c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                         593429 seqs, 438583890 residues
                                                                                                                  - nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Post-processing: Listing first 45 summaries
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Gapop 60.0 , Gapext 60.0
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Maximum DB seq length: 200000000
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                                                                                                                                                                                                                                                           Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                       Scoring table:
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RESULT

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Result No.	Score	Query Match	Query Match Length DB	DB	ID	Description
111	92	6.3	645		US-10-004-717-4	Sequence 4, Appli
7	92	6.3	861	σ	US-10-004-717-24	Sequence 24, Appl
m	92	6.3	1861	10	US-09-817-360-3	
4	32	2.2	5340	10	US-09-817-360-1	Sequence 1, Appli
'n	23	1.6	738	7	US-08-722-570-13	Sequence 13, Appl
9	23	1.6	790	6	US-10-004-717-20	Sequence 20, Appl
7	23	1.6	1385	σ	US-10-004-717-30	Sequence 30, Appl
80	23	1.6	1412	σ	US-10-004-717-6	ø
6	23	1.6	1412	σ	US-10-004-717-37	Sequence 37, Appl
c 10	20	٦. ۲.	352	10	US-09-728-445-108	Sequence 108, App
c 11	19	1.3	200	10	US-09-783-590-2157	Sequence 2157, Ap
c 12	19	1,3	1263	σ	US-09-938-842A-1036	Sequence 1036, Ap
13	18	1.2	4797	10	US-09-751-797-25	Sequence 25, Appl
c 14	18	1.2	20272	10	US-09-908-711-145	Sequence 145, App
c 15	18	1.2	25619	10	US-09-908-711-143	Sequence 143, App
c 16	18	1.2	25619	10	US-09-764-898-302	Sequence 302, App
c 17	18	1.2	31728	6	US-10-114-170-64	Sequence 64, Appl
18	18	1.2	402850	σ	US-09-844-653-5	Sequence 5, Appli
19	17	1.2	31	10	US-09-817-360-17	Sequence 17, Appl

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qq ò g US-10-004-717-24

RESULT

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	TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPEUTIC USE OF AN TITLE OF INVENTION: ACCORDANCE FOR DEARNESS, TITLE OF INVENTION: ACCORDANCE FOR DEARNESS, TITLE OF INVENTION: OSTEOARTHRITIS, AND ABNORMAL CELL PROLIFERATION FILE REFERENCE: PO1899084 CURRENT FILE REFERENCE: PO1899084 CURRENT FILING DATE: 2002-08-16 PRIOR APPLICATION NUMBER: 09/585,645 PRIOR FILING DATE: 2000-06-01 PRIOR FILING DATE: 1999-06-01 PRIOR FILING DATE: 2000-06-01 PRIO	0; Gaps	762 GCGCTGGATGCGCTGCGCGGTGTCCTGCCCACCTTCCCGGATGACCCCAACTTACAAAG 821
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	FER		TAC
	ESS COLI	\$ 5;	ACT
	SAFE	h 6 idel	CAA
	A DELLI	engt In	000
	COMPOSITIONS AND METHODS FOR THE THERAPEUTIC USE ATONAL ASSOCIATED SEQUENCE FOR DEAFNESS, OSTEOARTHRITIS, AND ABNORMAL CELL PROLIFERATION 99054 NUMBER: US/10/004,717 1002-08-16 MBER: US/85,645 000-06-01 MBER: 60/176,993 000-01-19 MBER: 60/177,060 999-06-01 : 69 er. 2.1	Ouery Match 6.3%; Score 92; DB 9; Length 645; Best Local Similarity 100.0%; Pred. No. 5.5e-39; Matches 92; Conservative 0; Mismatches 0; Indels	SOGCTGGATGCCTGCGCGGTGTCCTGCCCACCTTCCCGGATGACGCCAAACTTACAAG
	POI	9; 5e-1	2007 1111
	ABN	DB 5	1700 1000
	IETH ND 717	2; No. atc	CCT CCT
	3, A	e 9 d.	CCA
717	TITLE OF INVENTION: COMPOSITIONS AND METH TITLE OF INVENTION: ATONAL ASSOCIATED SE TITLE OF INVENTION: OSTEOARTHRITIS, AND FILE REFERENCE: PO1899US4 CURRENT APPLICATION NUMBER: US/10/004,717 CURRENT FILING DATE: 2002-08-16 FRIOR APPLICATION NUMBER: 09/585,645 PRIOR APPLICATION NUMBER: 09/585,645 PRIOR FILING DATE: 2000-06-01 PRIOR FILING DATE: 1999-06-01 PRIOR FILING DATE: 1999-06-01 FRIOR FILING DATE: 1999-06-01 FRIOR FILING DATE: 1999-06-01 FRIOR FILING DATE: 1999-06-01 FRIOR FILING DATE: 1999-06-01 TUMBER OF SEQ ID NOS: 69 EQ ID NO 4 LENGTH: 645 TYPE: DATE TYPE: DATE ORGANISM: MUS MUSCULUS 10-004-717-4	Pre	0517
004, A1	100N 10S/ 111 112 113		27.00
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e 4 tiol triol	OOF OOF THE APPLIES APPLIES OF THE	atc]	8 – 8
10-004-717-4 equence 4, Application US/ equence 4, Application US/ ublication No. US200201926 ENERAL INFORMATION: ENERAL INFORMATION: ADDITIONAL: ZOGHIL, HUDA Y.	TITLE OF INVENTION: COMPOSITIONS TITLE OF INVENTION: GCYECARTHRI TITLE OF INVENTION: GCYECARTHRI FILE REFERENCE: POL899US4 CURRENT APPLICATION NUMBER: US/1 CURRENT FILING DATE: 2002-08-16 PRIOR APPLICATION NUMBER: 60/176 PRIOR FILING DATE: 2000-01-19 PRIOR FILING DATE: 2000-01-19 PRIOR FILING DATE: 1999-06-01 PRIOR FILING DATE: 1999-06-01 WUMBER OF SEQ ID NOS: 69 LENGTH: 645 LENGTH: 645 LENGTH: 645 TYPE: DNA ORGANISM: MUS MUSCULUS	y M Lo hes	762 304
US-10-004-717-4 ; Sequence 4, Application US/10004717 ; Publication No. US20020192665A1 ; GENERAL INFORMATION: ; APPLICANT: ZOGENT GOGENT ; APPLICANT: COGENT ; APPLICANT: VANA CATANATION:	TITLE OF INV CURRENT APPLIC PRIOR PILING PRIOR PILING PRIOR FILING PRIOR FILING PRIOR FILING NUMBER OF SE SOFTWARE: PA SEQ ID NO 4 LENGTH: 645 TYPE: DNA US-10-004-717-4	uer sest latc	
US.	s -sn	OπΣ	QQ Db

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

1. /cgn2_6/ptodata/2/pubpna/USO7_PUBCOMB.seq:*
2. /cgn2_6/ptodata/2/pubpna/USO7_PUBCOMB.seq:*
3. /cgn2_6/ptodata/2/pubpna/USO6_NEW_PUB.seq:*
4. /cgn2_6/ptodata/2/pubpna/USO6_NEW_PUB.seq:*
5. /cgn2_6/ptodata/2/pubpna/USO6_NEW_PUB.seq:*
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14. /cgn2_6/ptodata/2/pubpna/USO0_PUBCOMB.seq:*
14. /cgn2_6/ptodata/2/pubpna/USO0_PUBCOMB.seq:*

Published_Applications_NA:*

Database :

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STRANDEDNESS:
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US-08-722-570-13
                                                                          -09-817-360-1
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                                                                APPLICANT: ZOGHBI, HUDA Y.

APPLICANT: ZOGHBI, HUDA Y.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPEUTIC USE OF AN TITLE OF INVENTION: OSTEOARTHRITS, AND ABNORMAL CELL PROLIFERATION STLE REFERENCE: POLSOBOUS4

TITLE OF INVENTION: OSTEOARTHRITS, AND ABNORMAL CELL PROLIFERATION STLE REFERENCE: POLSOBOUS4

CURRENT APPLICATION NUMBER: US/10/004,717

CURRENT FILING DATE: 2000-06-16

PRIOR FILING DATE: 2000-06-01

PRIOR FILING DATE: 2000-01-19

PRIOR APPLICATION NUMBER: 60/137,060

PRIOR PELLING DATE: 1999-06-01

NUMBER OF SEQ ID NOS: 69

SOFTWARE: PALENTIN VET. 2.1

SEQ ID NO 24

LENGTH: 861
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Sequence 3, Application US/09817360

Sequence 3, Application US/09817360

Sequence 3, Application US/09817360

SENERAL INCORMATION:
APPLICANT: German, Michael S.
APPLICANT: Lin, Joseph

TITLE OF INVENTION: PRODUCTION OF PANCREATIC ISLET CELLS

TITLE OF INVENTION: AND DELIVERY OF INSULIN
FILE REFERENCE: USF7-126CF

CURRENT APPLICATION NUMBER: US/09/817,360

CURRENT FILING DATE: 2000-03-20

PRIOR APPLICATION NUMBER: 69/535,145

PRIOR APPLICATION NUMBER: 60/128,180

PRIOR FILING DATE: 1999-04-06

NUMBER OF SEQ ID NOG: 19

SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 861;
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6.3%; Score 92; DB 9; Le
Best Local Similarity 100.0%; Pred. No. 5.4e-39;
Matches 92; Conservative 0; Mismatches 0;
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Sequence 24, Application US/10004717
Publication No. US20020192665A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
ORGANISM: Mus musculus
US-10-004-717-24
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; ORGANISM: Mus musculus
US-09-817-360-3
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Publication No. US20030044887A1

GENERAL INFORMATION:
APPLICANT: Anderson, David J.
APPLICANT: Anderson, David J.
TILLE OF INVENTION: NEUROGENIN
NUMBER OF SEQUENCES: 20
CORRESONDENCE ADDRESS: ADDRESSE: Four Embarcadero Center, Suite 3400

CITY: San Francisco
STATE: California
COUNTRY: United States
CONTRY: United States
                                            GENERAL INFORMATION:
APPLICANT: German, Michael S.
APPLICANT: German, Michael S.
TITLE OF INVENTION: PRODUCTION OF PANCHEATIC ISLET CELLS
TITLE OF INVENTION: AND DELIVERY OF INSULIN
FILE REFERENCE: UCSF-129CIP
CURRENT APPLICATION NUMBER: US/09/817,360
CURRENT FILING DATE: 2001-03-20
PRIOR APPLICATION NUMBER: 09/535,145
PRIOR APPLICATION NUMBER: 60/128,180
PRIOR APPLICATION NUMBER: 60/128,180
PRIOR FILING DATE: 1999-04-06
NUMBER OF SEQ ID NOS: 19
SOFTWARE: FastsEQ for Windows Version 4.0
SEQ ID NO 1
LENGTH: 5340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTE READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/722,570
FILING DATE: 27-SEP-1996
CLASSIFICATION: 5365
ATTORNEY/AGENT INFORMATION:
NAME: Silva, RObin M.
REGISTRATION NUMBER: 38,304
FREGISTRATION NUMBER: 38,304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 2.2%; Score 32; DB 10; Best Local Similarity 100.0%; Pred. No. 4.9e-07; Matches 32; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: A-63902/RFT/RMS
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3235 AAGAGGGAGTTGGCACTGAGCAAGCAGCGACG 3266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           672 AAGAGCGAGTTGGCACTGAGCAAGCAGCGACG 703
Sequence 1, Application US/09817360 Patent No. US20020015696A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELERAX: (415) 398-3249
TELEX: 910 277299
INFORMATION FOR SEQ ID NO: 13:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: (415) 781-1989
TELEFAX: (415) 398-3249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 738 base pairs TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
CORGANISM: Homo Sapiens
US-09-817-360-1
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TYPE: DNA.
CORGANISM: Mus musculus
US-10-004-717-6
; ORGANISM: Mus musculus US-10-004-717-30
                                                                                                                                                                                                                                        RESULT 8
US-10-004-717-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         qq
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Sequence 20, Application US/10004717

Sequence 20, Application US/10004717

Sequence 20, Application No. 10220192665A1

GENERAL INFORMATION:

APPLICANT: ZOGHBI, HUDA Y.

APPLICANT: YANG, QI

TITLE OF INVENTION: ATONAL ASSOCIATED SEQUENCE FOR DEAFNESS,

CURRENT APPLICATION NUMBER: 05/10/004,717

PRIOR FILING DATE: 2000-06-01

PRIOR FILING DATE: 2000-06-01

PRIOR FILING DATE: 2000-06-01

PRIOR PELIORATION NUMBER: 60/176,993

PRIOR PELIORATION NUMBER: 60/176,993

PRIOR FILING DATE: 1999-06-01

NUMBER OF SEQ ID NOS: 69

SEQ ID NO 20

MANDER OF SEQ ID NOS: 69

LENGTH: 790

MANDER OF SEQ ID NOS: 69

LENGTH: 790
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1.6%; Score 23; DB 9; Length 790;
Best Local Similarity 100.0%; Pred. No. 0.038;
Matches 23; Conservative 0; Mismatches 0; Indels
                                                                             Length 738;
                                                                           Query Match 1.6%; Score 23; DB 7; Length 736
Best Local Similarity 100.0%; Pred. No. 0.038;
Matches 23; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                               304 GAGCGCAACCGCATGCACCACCT 326
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                                                                                                                                                        732 GAGCGCAACCGCATGCACAACCT 754
                    ; MOLECULE TYPE: DNA US-08-722-570-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
CRGANISM: chicken
US-10-004-717-20
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US-10-004-717-30
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Sequence 6, Application US/10004717

| Sequence 6, Application US/20020192665A1
| Publication No. US20020192665A1
| GENERAL INFORMATION:
| APPLICANT: ZOGHEI, HUDA Y.
| APPLICANT: ZOGHEI, HUDA Y.
| TITLE OF INVENTION: OCHOOSITIONS AND METHODS FOR THE THERAPEUTIC USE OF AN TITLE OF INVENTION: OCHOOSITIONS AND METHODS FOR THE THERAPEUTIC USE OF AN TITLE OF INVENTION: OCHOOSITIONS AND ABNORMAL CELL PROLIFERATION FILE REFERENCE: P01899US4
| CURRENT FILING DATE: 2000-08-16
| CURRENT FILING DATE: 2000-06-01
| PRIOR FILING DATE: 2000-01-19
| PRIOR FILING DATE: 2000-01-19
| PRIOR PELICATION NUMBER: 60/137,060
| PRIOR FILING DATE: 1999-06-01
| NUMBER OF SEQ ID NOS: 69
| SEQ ID NO 6
| SEQ ID NO 6
| LENTH: 1412
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OKENT 91

Sequence 37, Application US/10004717

Sequence 37, Application US/20020192665A1

GENERAL INFORMATION:

APPLICANT: ZOGHBI, HUDA Y.

APPLICANT: YANG, OI

TITLE OF INVENTION: ACONEOSITIONS AND METHODS FOR THE THERAPEUTIC USE OF AN

TITLE OF INVENTION: ACONEOSITIONS AND ABNORMAL CELL PROLIFERATION

TITLE OF INVENTION: ACONEOSITIONS AND ABNORMAL CELL PROLIFERATION

FILE REFERENCE: P018990TG4

CURRENT FILING DATE: 2000-06-01

PRIOR FILING DATE: 2000-06-01

PRIOR FILING DATE: 2000-06-01

PRIOR FILING DATE: 1000-01-19

PRIOR FILING DATE: 1999-06-01

PRIOR FILING DATE: 1999-06-01

NUMBER OF SEQ ID NOS: 69

SOFTWARR: PATENTION VERENT: 60/137,060

NUMBER OF SEQ ID NOS: 69

SOFTWARR: PATENTIN VERENT: 1999-06-01

SOFTWARR: PATENT: 1999-06-01

SOFTWARR: PATENTIN VERENT: 1999-06-01
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    Length 1385;
                                                                                             0; Indels
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    DB 9;
0.036;
Query Match 1.6%; Score 23; DB Best Local Similarity 100.0%; Pred. No. 0.C Matches 23; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           445 GAGCGCAACCGCATGCACAACCT 467
                                                                                                                                                                                                                                    742 GAGCGCAACCGCATGCACAACCT 764
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LOCATION:
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APPLICANT: Dillon, Patrick J.
APPLICANT: Haseltine, William A.
APPLICANT: Haseltine, William A.
APPLICANT: Li, Hacdong
APPLICANT: Rosen, Craig A.
APPLICANT: Ruben, Steven M.
ITILE OF INVENTION: Human Genes, Sequences, and Expression Products 16.2
FILE REFERENCE: PO-16.2Cl
CURRENT APPLICATION NUMBER: 08/420,856
PRIOR FILING DATE: 1995-04-12
PRIOR FILING DATE: 1995-04-12
PRIOR FILING DATE: 1994-11-21
NUMBER OF SEQ ID NOS: 12485
SOFTWARE PATENTIN VET. 2.0
SOFTWARE PATENTIN VET. 2.0
SEQ ID NO 2157
LENGTH: 500
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                                                                                          Gaps
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APPLICANT: Sands, Arthur T.
TITLE OF INVENTION: NO. US20020102543Alel Mutated Mammalian Cells and
TITLE OF INVENTION: Animals
FILE REFERENCE: LEX-0102-USA
CURRENT APPLICATION NUMBER: US/09/728,445
CURRENT FILING DATE: 2000-11-30
PRIOR FILING DATE: 1999-12-01
NUMBER OF SEQ ID NOS: 891
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 108
LENTH: 352
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                                        Query Match 1.6%; Score 23; DB 9; Length 1412; Best Local Similarity 100.0%; Pred. No. 0.036; Matches 23; Conservative 0; Mismatches 0; Indels
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1.6;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 1.4%; Score 20; DB Best Local Similarity 100.0%; Pred. No. 1.6 Matches 20; Conservative 0; Mismatches
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LOCATION: (84)
OTHER INFORMATION: n equals a,t,g, or
NAME/KEY: misc feature
LOCATION: (207)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-783-590-2157/c
; Sequence 2157, Application US/09783590
; Patent No. US20020110850A1
                                                                                                                                                                                                                                                                           Sequence 108, Application US/09728445 Patent No. US20020102543A1 GENERAL INFORMATION: APPLICANT: Friedrich, Glenn
                                                                                                                              732 GAGCGCAACCGCATGCACAACCT 754
                                                                                                                                                    445 GAGCGCAACCGCATGCACAACCT 467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; TYPE: DNA
; ORGANISM: Mus musculus
US-09-728-445-108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
ORGANISM: Homo saplens
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
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US-09-728-445-108/c
US-10-004-717-37
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RESULT 12
US-09-938-842A-1036/c
US-09-938-842A-1036/c
| Sequence 1036, Application US/09938842A
| Sequence 1036, Application US/09938842A
| Setent No. US2020166378A1
| GENERAL INFORMATION:
| APPLICANT: Harper, Joef |
| APPLICANT: Harper, Joef |
| APPLICANT: And, Xun |
| APPLICANT: Zhu, Tong |
| TITLE OF INVENTION: STAME, AND METHODS OF USE |
| TITLE OF INVENTION: SAME, AND METHODS OF USE |
| FILE REPERENCE: SCRIP1300-3 |
| CURRENT APPLICATION NUMBER: US/09/938,842A |
| CURRENT FILING DATE: 2001-08-24 |
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Pred. No. 5.4;
Mismatches 0;
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (441)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: US 60/227,866
PRIOR FILING DATE: 2000-08-24
PRIOR PELLING DATE: 2001-01-16
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/300,111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LOCATION: (418)
OTHER INFORMATION: n equals a,t,g, or NAME/KEY: misc feature
LOCATION: (439)
OTHER INFORMATION: n equals a,t,g, or
                                                                                                                                                                                          OTHER INFORMATION: n equals a,t,g, or NAME/KEY: misc feature LOCATION: (360)
                                                                                                                                                                                                                                                             or
                                                         OTHER INFORMATION: n equals a,t,g, or NAME/KEY: misc feature
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OTHER INFORMATION: n equals a,t,g, or
                                                                                               LOCATION: (324)
OTHER INFORMATION: n equals a,t,g,
NAME/KEY: misc feature
                                                                                                                                                                                                                                                                                                                                                                                                                                 LOCATION: (379)
OTHER INFORMATION: n equals a,t,g,
NAME/KEY: misc feature
OTHER INFORMATION: n equals a,t,g,
NAME/KEY: misc feature
                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: n equals a,t,g,
NAME/KEY: misc feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LOCATION: (411)
OTHER INFORMATION: n equals a,t,g,
NAME/KEY: misc feature
                                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION: n equals a,t,g,
                                                                                                                                                                                                                                                      OTHER INFORMATION: n equals a,t,g,
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Best Local Similarity 100.0%; Pi
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Query Match 1.2%; Score 18; DB 10; Length 20272; Best Local Similarity 100.0%; Pred. No. 13; Matches 18; Conservative 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR FILING DATE: 2001-01-17
PRIOR PELICATION NUMBER: 09/764,874
PRIOR PELICATION NUMBER: 09/764,874
PRIOR APPLICATION NUMBER: 09/764,874
PRIOR PELING DATE: 2001-01-17
PRIOR PELING DATE: 2001-01-17
PRIOR PELING DATE: 2001-01-17
PRIOR PELING DATE: 2001-01-17
PRIOR APPLICATION NUMBER: 09/764,853
PRIOR APPLICATION NUMBER: 09/764,902
PRIOR PILING DATE: 2001-01-17
PRIOR APPLICATION NUMBER: 09/764,902
PRIOR PILING DATE: 2001-01-17
PRIOR APPLICATION NUMBER: 09/764,902
PRIOR PILING DATE: 2001-01-17
PRIOR PELING DATE: 2001-01-17
PRIOR APPLICATION NUMBER: 09/764,864
PRIOR FILING DATE: 2001-01-17
PRIOR PELING DATE: 2001-01-17
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PRIOR FILING DATE: 2001-01.17
PRIOR FILING DATE: 2001-01.17
PRIOR FILING DATE: 2001-01.17
PRIOR APPLICATION NUMBER: 60/179,065
PRIOR APPLICATION NUMBER: 60/180,628
PRIOR FILING DATE: 2000-01.31
PRIOR APPLICATION NUMBER: 60/180,628
PRIOR FILING DATE: 2000-02-04
PRIOR PRILING DATE: 2000-06-07
NUMBER OF SEQ ID NOS: 167
SOFTWARR: PALENTIN VET: 2.0
SEQ ID NO 145
LENGTH: 20272
                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: USO1/01339
PRIOR FILING DATE: 2001-01-17
PRIOR APPLICATION NUMBER: 09/764,869
PRIOR FILING DATE: 2001-01-17
PRIOR APPLICATION NUMBER: US01/01340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR FILING DATE: 2001-01-17
PRIOR APPLICATION NUMBER: US01/01336
PRIOR FILING DATE: 2001-01-17
                                                                                            PRIOR FILING DATE: 2001-01-17
PRIOR APPLICATION NUMBER: US01/01354
PRIOR FILING DATE: 2001-01-17
PRIOR APPLICATION NUMBER: 09/764,891
PRIOR FILING DATE: 2001-01-17
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CRCANISM: Homo sapiens
US-09-908-711-145
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Petent NO. US20010024652A1

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Dumoutier, Laure
APPLICANT: Dumoutier, Laure
APPLICANT: Louhed, Jamila
APPLICANT: Louhed, Jamila
APPLICANT: Louhed, Jamila
APPLICANT: Louhed, Jamila
APPLICANT: Remaild, Jamila
APPLICANT: Remaild, Jamila
APPLICANT: NOWERTION: (TIFS) The Proteins Encoded, and Uses Thereof
TITLE OF INVENTION: (TIFS) The Proteins Encoded, and Uses Thereof
TILE REFERENCE: LUD 5543.2
CURRENT APPLICATION NUMBER: US/09/751,797
CURRENT FILING DATE: 1999-10-18
PRIOR FILING DATE: 1999-10-26
PRIOR FILING DATE: 1998-10-26
PRIOR FILING DATE: 1998-10-26
PRIOR FILING DATE: 1998-10-26
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; Sequence 145, Application US/09908711
; Patent No. US20020045230A1
; GREERAL INFORMATION:
    APPLICANT: Rosen et al.
    TITLE OF INFORMION:
    TILE REPERENCE: PAL28
    CURRENT FILING DATE: 2001-07-20
    PRIOR APPLICATION NUMBER: US/09/908,711
CURRENT FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: US01/01360
; PRIOR APPLICATION NUMBER: US01/01344
; PRIOR FILING DATE: 2001-01-17
; PRIOR PILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: US01/01345
; PRIOR APPLICATION NUMBER: US01/01345
; PRIOR APPLICATION NUMBER: US01/01-17
; PRIOR PILING DATE: 2001-01-17
; PRIOR PILING DATE: 2001-01-17
; PRIOR PILING DATE: 2001-01-17
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15;
                                                                                                                                                                                                                                                        1.3%; Score 19; DB 9; Length 1263;
100.0%; Pred. No. 4.9;
Live 0; Mismatches 0; Indels
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                                                                                                                                 ; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-938-842A-1036
                                                                                                                                                                                                                                                                                                                                                                                      658 GGCGCAACAGGCCCAAGAG 676
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                                                                                                                                                                                                                                                                                                                                                                                                                          599 GGCGCAACAGGCCCAAGAG 581
PRIOR FILING DATE: 2001-06-22 NUMBER OF SEQ ID NOS: 5379 SEQ ID NO 1036
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 2001-01-1
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Best Local Similarity 100.0
Matches 18; Conservative
                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 100.(
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
ORGANISM: Homo sapiens
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US-09-908-711-145/c
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US-09-751-797-25
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LENGTH: 4797
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Query Match 1.2%; Score 18; DB 10; Length 25619; Best Local Similarity 100.0%; Pred. No. 13; Matches 18; Conservative 0; Mismatches 0; Indels 0;
                PRIOR APPLICATION NUMBER: 0001/01-17
PRIOR PELING DATE: 2001-01-17
PRIOR FILING DATE: 2001-01-17
PRIOR FILING DATE: 2001-01-17
PRIOR FILING DATE: 2001-01-17
PRIOR PELICATION NUMBER: 0501/01312
PRIOR PELING DATE: 2001-01-17
PRIOR PELING DATE: 2000-01-31
PRIOR PELING DATE: 2000-01-31
PRIOR PELING DATE: 2000-02-04
PRIOR FILING DATE: 2000-02-04
PRIOR FILING DATE: 2000-02-04
PRIOR FILING DATE: 2000-06-07
NUMBER OF SEQ ID NOS: 167
SOFTWARE: PATENTIN NUMBER: 60/209/467
PRIOR PLING DATE: 2000-06-07
NUMBER OF SEQ ID NOS: 167
SEQ ID NO 143
LENGHI 25619
                                                                                                                                                                                                                                                                                                                                                                  Search completed: April 8, 2003, 21:14:29
Job time: 291 secs
                                                                                                                                                                                                                                                                                                        QY 1153 TCAGAGCTGTCTGAAATG 1170
                                                                                                                                                                                                                                                                                                                        1048 TCAGAGCTGTCTGAAATG 1031
                                                                                                                                                                                                         TYPE: DNA
CORGANISM: Homo sapiens
US-09-908-711-143
                                                                 PRIOR FILING DATE: 2001-117
PRIOR APPLICATION NUMBER: 09/764,896
PRIOR FILING DATE: 2001-01-17
PRIOR APPLICATION NUMBER: US01/01307
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RIOR APPLICATION UNDBER: 09/764,864
RRIOR FILING DATE: 2001-01-17
PRIOR APPLICATION NUMBER: US01/01341
6642 TCAGAGCTGTCTGAAATG 6625
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US-09-908-711-143/c
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Gaps

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1. .962
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Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCACGAG(G). Library constructed by
Ling Hong in the laboratory of Gerald M. Rubin (University
of California, Berkeley) using ZAP-CDNA synthesis Xit
(Stratagene) and Superscript II RT (Life Technologies).
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AGENCOURT_8340711 NIH_MGC_110 Homo sapiens cDNA clone IMAGE:6249314
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NIH-MGC http://mgc.nci.nih.gov/.

NIH-MGC http://mgc.nci.nih.gov/.

NIH-MGC http://mgc.nci.nih.gov/.

L Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-rémail.nih.gov

Tissue Procurement: Arc.

CDNA Library Preparation: Rubin Laboratory

CDNA Library Preparation Laboratory

CDNA Library Preparation Laboratory

CDNA Library Prepar
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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100.0%; Pred. No. 19;
iive 0; Mismatches 0; Indels
                                        Length 953;
                                    Query Match 1.4%; Score 21; DB 9; Best Local Similarity 100.0%; Pred. No. 19; Matches 21; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                     5', mRNA sequence.
BQ686909
BQ686909.1 GI:21812225
                                                                                                                                                                729 CGGGAGCGCAACCGCATGCAC 749
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/lab_host="labdomyosarcoma"
/lab_host="labdomyosarcoma"
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Site_2: XhoI; cDNA made by oligo-dT priming.
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for average insert size 1:8kb. Library constructed by
Ling Hong in the laboratory of Gerald M. Rubin (University
of California, Berkeley) using ZaP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
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was primed with an oligo(dT) primer
was primed with an oligo(dT) primer
ATGTGGCCTTTTTTTTTTTTTTT]; double-stranded cDNA was
ligated to a DraIII adaptor [TGTTGGCCTACTGG], digested and
cloned into distinct braiII sites of the pME18S-FL3. XhoI
sites just outside the DraIII sites can be used to isolate
the cDNA insert. Size selection was performed to exclude
fragments <1.5 kb. Library was constructed by Sugano et
al.(University of Tokyo, Institute of Medical Science).
Custom primer used for sequencing: 5' end primer
[CGACTGCCTGCAGAGCACG], 3' end primer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. E 1 (bases 1 to 953)
E 1 (bases 1 to 953)
S Hashimoto K., Kusuda, J., Tanuma, R., Ito, A., Hirata, M., Toyoda, A., Suzuki, Y., Sasaki, M. and Sugano, S.
Isolation of full-length cDNA clones from a mouse brain cDNA library made by oligo-capping method
Unpublished (1999)
Contact: Katsuyuki Hashimoto
Division of Genetic Resources
National Institute of Infectious Diseases
23-1, Toyama I chome, Shinjuku-ku, Tokyo 162-8640, Japan
Email: khashi@inly@o.jp/yoken/genbank/.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AU067624 Sugano mouse brain mncb Mus musculus cDNA clone MNCb-3693 5', mRNA sequence.
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ORGANISM
Homo sapiens
Extravolar Metacas. Chordata; Craniata; Vertebrata; Euteleostomi;
Marmalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHONS
AUTHONS
NIH-MCC http://mgc.nci.nih.gov/
TITLE
NATIONALL Contact: Robert Strausberg, Ph.D.
COMMENT
CONTACT: Robert Strausberg, Ph.D.
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CONTACT: Robert Strausberg, Ph.D.
CONTACT: Robert Strausperg, Ph.D.
FEATURES

I. 1022
Contact: Robert Strausperg, Ph.D.
Alab.Dost-*Homo sapiens*
Abaret **Lobert Strausperg, Ph.D.
Abaret **Lobert Strausperg, Ph.D.
CONTACTIONAL STRAUSPERG, Abaret Strausperg, Ph.D.
Alab.Dost-*Homo sapiens*
Alab.Do
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Db 573 AACAGGCCCTGGGCGGTGGGC 593
Search completed: April 8, 2003, 21:09:45
Job time: 2284 secs

1112 AACAGGCCCTGGGCGGTGGGC 1132

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Query Match
1.4%; Score 21; DB 13; Length 1022;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 21; Conservative 0; Mismatches 0; Indels

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8, 2003, 05;44:40 ; Search time 4064 Seconds (without alignments) 10455.240 Million cell updates/sec
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GenCore version 5.1.4_p5_4578 Copyright <a href="mailto:right-4">(c) 1993 - 2003 Compugen Ltd.</a>
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                                                                                                                                                                                                                                               2054640 seqs, 14551402878 residues
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em_htgo_hum:*
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is the number of results predicted by chance to have a

Pred. No.

em_htgo_other:*

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PGGGSSGDWGSIYSPYSQAGSLSPTALEEFPGLQVPSSPSCLLPGTLVFSDFL"
487 c 413 g 284 t
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                                                                                                                A91167 Sequence 1
Y10619 R.norvegicu
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Patent: WO 9827206-1 22-JUN-1998;
ICARD LIEPKALNS CHRISTINE (FR); MALLET JACQUES (FR)
LOCATION/Qualifiers
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Pred. No. 0;
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A91167
                                               SUMMARIES

    1491
    /organism="Rattus sp."
    /db_xref="taxon:10118"

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ilarity 100.0%;
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/SIGNIE # #12 | #12 | #12 | #12 | #12 | #12 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #13 | #1
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R.norvegicus mRNA for transcriptional regulator, Relax.
Y10619
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
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Ravassard, P., Chatail, F., Mallet, J. and Icard-Liepkalns, C.
Relax, a novel rat bHLH transcriptional regulator transiently
expressed in the ventricular proliferating zone of the developing
central nervous system
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Submitted (20-JAN-1997) P. Ravassard, CNRS UMR 9923, Bat. CERVI,
Hopital de la Pitie Salpetriere, 83 Bd. de l'Hopital, F-75013
Paris, FRANCE
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7. cranism="Rattus norvegicus" /strain="Wistar"
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Rattus norvegicus.
Rattus norvegicus
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1441 AGAGTGACCTAATCCAGTGT 1460
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Ravassard, P.
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                    CGCCCACCATCCAAGTGTCCCAAGAGCCCAGCAACCCTTTCCCGGAGCCTCGGACCACG
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OM nucleic

Run on:

Sequence:

Searched:

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Basic helix-loop-helix; BHLH; RELAX; Rat Embryonic Longitudinal Axis; control; gene expression; transcriptional activator; targeting; protein expression; central nervous system; CNS; treatment; nervous system disorder; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Basic helix-loop-helix polypeptide and related nucleic acid - w transcriptional activity, for targeting expression of genes to central nervous system and treatment of nervous disease
                                                                                              cDNA encoding a novel BHLH protein designated RELAX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mallet J, Ravassard P, Icard-Liepkalns C;
                                                                                                                                                                                                                                                                                                 Location/Qualifiers
459..1103
/*tag= a
/product= RELAX
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                      GenCore version 5.1.4\_p5\_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
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length: 2000000000
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The present sequence encodes a basic helix-loop-helix (BHLH) type protein, designated RELAX (Rat Embryonic Longitudinal Axis) protein. The protein is used to control and participate in gene expression, by acting as transcriptional activator, strictly dependent on the presence of an intext E box (CANNTG), particularly for targeting expression of proteins to the central nervous system (CNS). The nucleic acid sequence can be used to treat nervous system disorders, and antisense sequences can be used to control mRNA transcription.
                                                                                                                                                                                                                                                                                                                                         1 GCAGGTAGCGAGAGGAGCAGTCCCTGGGCCCCCGTTGCTGATTGGCCCGTGGCACAGGCA
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ALIGNMENTS

AAV42512 standard; cDNA; 1491 BP

RESULT 1 AAV42512 ID AAV4

1491 19 AAV42512

1460 100.0

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                                TAGAAGAGGGAGTGGGTGGGCGTACTCTAGTCCCGCGTGGAGTGACCTCTAAGTCAGAG
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Db 1441 AGAGTGACCTAATCCAGTGT 1460

Search completed: April 8, 2003, 11:37:01 Job time : 374 secs us-09-595-947c-1_2.rnpb

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GenCore version 5.1.4_p5_4578
Copyright*(c) 1993 - 2003 Compugen Ltd.
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OM nucleic - nucleic search, using sw model

April 8, 2003, 11:23:35 ; Search time 122 Seconds (without alignments) 10497.254 Million cell updates/sec 1 gcaggtagcgagaggagcag......agagtgacctaatccagtgt 1460 US-09-595-947C-1 1460 Title: Perfect score: Sequence: Run on:

IDENTITY_NUC Gapext 1.0 Scoring table:

Total number of hits satisfying chosen parameters:

593429 seqs, 438583890 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 80% Maximum Match 100% Listing first 45 summaries

cgn2_6/ptodata/2/pubpna/USO7_PUBCOMB.seq:*

cgn2_6/ptodata/2/pubpna/USO6_NEW_PUB.seq:*

cgn2_6/ptodata/2/pubpna/USO6_NEW_PUB.seq:*

cgn2_6/ptodata/2/pubpna/USO6_NEW_PUB.seq:*

cgn2_6/ptodata/2/pubpna/USO7_NEW_PUB.seq:*

cgn2_6/ptodata/2/pubpna/USO8_NEW_PUB.seq:*

cgn2_6/ptodata/2/pubpna/USO8_NEW_PUB.seq:*

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cgn2_6/ptodata/2/pubpna/USO8_NEW_PUB.seq:*

cgn2_6/ptodata/2/pubpna/USO8_NEW_PUB.seq:*

cgn2_6/ptodata/2/pubpna/USO9_NEW_PUB.seq:*

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cgn2_6/ptodata/2/pubpna/USO9_NEW_PUB.seq:* /cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq:*/cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*/cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:* Published_Applications_NA:* 12: 13: Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description Query Score Match Length DB Result

No matches found

Search completed: April 8, 2003, 18:58:39
Job time: 124 secs

us-09-595-947c-1_2.rst

```
GenCore version 5.1.4_p5_4578 Copyright*(c) 1993 - 2003 Compugen Ltd.
```

OM nucleic - nucleic search, using sw model

April 8, 2003, 06:37:40 ; Search time 2258 Seconds (without alignments) 10471.838 Million cell updates/sec 1 gcaggtagcgagaggagcag.....agagtgacctaatccagtgt 1460 US-09-595-947C-1 1460 Title: Perfect score: Sequence: Run on:

16154066 seqs, 8097743376 residues IDENTITY_NUC Gapext 1.0 Scoring table: Searched:

Total number of hits satisfying chosen parameters: Post-processing: Minimum Match 80% Maximum Match 100% Listing first 45 summaries Minimum DB seq length: 0 Maximum DB seq length: 2000000000

EST:* Database :

gb_est3:*
gb_est4:*
em_estfun:*
em_estfun:*
em_gss:*
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em_gss_hum:*
em_gss_hut:* em_estba:*
em_esthum:*
em_estin:*
em_estin:* em_estov:*
em_estpl:*
em_estro:*
em_htc:*
gb_estl:* gb_est2: gb_htc:*

em_gss_mam:* em_gss_mus:* em_gss_other:* em_gss_rod:* em_gss_fun:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description Query Score Match Length DB ID Result ٠ و

No matches found

Search completed: April 8, 2003, 17:56:21 Job time: 2258 secs

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BI910102 603067946
BR504175 601867625
BOG686904 AGENCOURT
BM563662 AGENCOURT
BM563662 AGENCOURT
BM763620 601469349
BG419220 602469349
BG419220 602469349
BG419220 602469349
BG419220 602469349
BM713743 WSF Pyroc
T70947 yc49c05.r1
BH445873 da133c04.A
AV933697 AV934801
BM233695 514449 MA
AV939670 AV939670
AL173398 TETRACOON
BM219506 TETRACOON
BM810917 AGENCOURT
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BF191528 230410L20
ACST600 AM057600
BM030260 AU057600
BM030260 AU057600
BM030261 AU1_91_G1
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RPCI-23-160G18.TV RPCI-23 Mus musculus genomic clone RPCI-23-160G18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          That is a superman, which is the superman, s., Athret Jacobs., Nierman, W., Feldblyum, T., Malek, J., Shatsman, S., Akinret J., Levins, M., Mcgann, S., Tsegaye, G., Geer, K., Krol, M., de Jong, P. and Fraser, C.M.

Mouse BAC End Sequences from Library RPCI-23
Unpublished (1999)
Other. GSSS: RPCI-23-160318.TJ
Contact: Shaying Tabonics
The Institute for Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
The: 301 838 0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chordata; Craniata; Vertebrata; Euteleostomi; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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BB269747
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BF191528
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RESULT 1
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10462.571 Million cell updates/sec
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                                                                                                    April 8, 2003, 17:16:22; Search time 2260 Seconds
                                                                                                                                                                                                                                                                                                                                      31743302
            GenCore version 5.1.4\_p5\_4578 Copyright \cite{C} 1993 - 2003 Compugen Ltd.
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                                                                                                                                                                                                                                                                        16154066 seqs, 8097743376 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUMMARIES
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                                                                         nucleic search, using sw model
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Gapop 60.0 , Gapext 60.0
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Minimum DB seq length: 0 Maximum DB seq length: 200000000

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Word size :

Searched:

em_esthum:
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em_esto:*
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em_gss_hum:

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em_estfun: em_estom:* em_gss_pln:

em_gss_fun: em_gss_mus: em_gss_pro: em_gss_rod:

em_gss_

em_gss_mam:

US-09-595-947C-1 1460

Perfect score:

Sequence:

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:uo

Scoring table:

Email: szhao@tigr.org Clones are derived from the mouse BAC library RPCI-23. For BAC library availability, please contact Pieter de Jong (pieter@dejong.med.buffalo.edu). Clones may be purchased from

AZ296526 RPCI-23-1 AK008017 Mus muscu BG808248 2083-52 M AL540071 AL540071 BQ178789 UT.M-EV0-BG854922 1024041C0

AK008017 BG808248 AL540071 BQ178789 BG854922

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                                                                                                                                                                                                                                                                                                                                           /note="Organ: Kidney/Brain; Vector: pBACe3.6; Site_1:
Coorl: Site_2: Ecorl: Female C57BL65 mouse kidney and/or
brain genomic DNA was isolated and partially digested
with a combination of Ecorl and Ecorl Methylase. Size
selected DNA was cloned into the pBACe3.6 vector at the
ECORI sites. The ligation products were transformed into
DH109_electrocompetent cells (BRL Life Technologies)."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
BACPAC Resources (http://bacpac.med.buffalo.edu/orderingframe.htm) or from Resea ch Genetics (info@resgen.com). BAC end page: http://www.tigr.ofg/tdb/bac_ends/mouse/bac_end_intro.html plate:ifo row: G column: 18 Seg primer: T7 Class: BAC ends.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus adult male small intestine cDNA, RIKEN full-length enriched library, clone:2010001M19:atonal homolog 5 (Drosophila), full insert sequence.
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HTC: CAP trapper.
Mus musculus (strain:C57BL/6J) adult male small intestine cDNR
mNA, clone_lib:RIKEN full-length enriched mouse cDNA library
clone:2010001M19.
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.00.0%; Pred. No. 4.8e-37;
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High efficiency full-length cDNA cloning
Weth. Enzymol. 303, 19-44 (1999)
99279253
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live 0; Mismatches
                                                                                                                                                                            /organism="Mus musculus"
/strain="c57BL/6J"
/db_xref="taxon:10090"
/clone="RPCI-23-160G18"
/clone_lib="RPCI-23"
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                                                                                                                                    Location/Qualifiers
1. .593.
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                                                                                                                                                                                                                                                                                                     /sex="Female"
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Rawai, J., Shinagawa, A., Shibata, K., Yoshino, M., Itoh, M., Ishii, Y., Arakawa, T., Hara, A., Fukunishi, Y., Konno, H., Adachi, J., Fukuda, S., Arakawa, M., Nishi, K., Xiyosawa, H., Kondo, S., Yamanaka, I., Saito, T., Saito, T., Saito, T., Saito, T., Saito, T., Saito, R., Kaota, T., Saito, R., Kadota, K., Matsuda, H., Ashburner, M., Batalov, S., Casavant, T., Fleischman, M., Gasterland, T., Gissi, C., King, B., Kochlwa, H., Kuehl, P., Lewis, S., Matsuo, Y., Mikaldo, I., Pesole, G., Kochlwa, H., Wanner, J., Schriml, L.M., Staubli, F., Suzuki, R., Tomita, M., Wanner, L., Washlo, T., Sakai, K., Okido, T., Furuno, M., Aono, H., Baldarelli, R., Barsh, G., Blake, J., Boffelli, D., Bojunga, N., Carninci, P., de Bonaldo, M. F., Brownstein, M.J., Bult, C., Fletcher, C., Fujita, M., Gariboldi, M., Gustincich, S., Hill, D., Hofmann, M., Hume, D. A., Kamiya, M., Lee, N. H., Lyons, P., Narchionni, L., Mashima, J., Mazzarelli, J., Mombaerts, P., Nordone, P., Ring, B., Ringwald, M., Rodriguez, I., Sakamoto, N., Sasaki, H., Sato, K., Schondach, C., Seya, T., Shibata, Y., Storch, K.F., Suzuki, H., Toyo-oka, K., Wang, K.H., Weitz, C., Whittakar, Y., Storch, K.F., Suzuki, Y., Functional annotation of a full-length mouse cDNA collection NE. 1005560
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "." Adachi.J., Alzawa.K., Akahira.S., Akimura.T., Aono.H., Arai.A.,
Arakawa.T., Baldarelli.R., Bono.H., Brownstein,M., Bult.C.,
Carninci,P., Fukuda.S., Fukunishi.Y., Furuno.M., Hanagaki.T.,
Hara.A., Hayata.N., Hill.D., Hiramoto.K., Hiraoka.T., Hori.F.,
Hume.D., Imotani.K., Ishii.Y., Itoh,M., Izawa.M., Kasukawa.T.,
Kato.H., Kawai.J., Kojima.Y., Konno.H., Kouda.M., Koya.S.,
Kurihara.C., Matsuyama.T., Miyazaki.A., Nishi.K., Nomura.K.,
Numazaki.R., Ohno.M., Okazaki.Y., Okido.T., Owa.C., Quackenbush.J.,
Saito.H., Saito.R., Sakai.C., Sakai.K., Sano.H., Sasaki.D.,
Sohrimi.L., Shibata.K., Shibata.Y., Shinagawa.A., Takahashi.F.,
Tanaka.T., Tejima.Y., Tagami.M., Tagawa.A., Takahashi.F.,
Yasunishi.A., Yoshida.K., Yoshino.M., Muramatsu.M. and
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Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. First strand cDNA was primed with a primer [5, GAGAGAGAGATCCAAGAGCTTTTTTTTTTTTTTTYN 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of normalization to Rot = 5.0 and subtraction to Rot = 20.0. Second strand cDNA was prepared with the primer adapter
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Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of Submitted (10-JUL-2000) For Submitted (10-JUL-2000) Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Gemomic Sciences Center (GSC), RIKEN Yokohama Institute; 1--22 Submission-or Tsuumi-ku, Yokohama, URL: http://genome_15c.riken_19-1p/, Tel:81-45-503-9222, Fax:81-45-503-9216)
Please visit our web site (http://genome.gsc.riken.go.jp/) for further details.
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Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y. RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer Genome Res. 10 (11), 1757-1771 (2000)
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/organism="Mus musculus"
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Gaps

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo. Manmalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. I (bases 1 to 804)

E Li,W.B., Gruber,C., Jessee,J. and Polayes,D. Full-length cDNA libraries and normalization

L Unpublished (2001)

Contact: Genoscope Genoscope Genoscope Genoscope - Centre National de Sequencage

BP 191 91006 EVRX cedex - France

Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr.

Location/Qualifiers

I. 804
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Anote-Torgan: Fetal brain; Vector: pCMVSPORT 6; 1st strand CDNA was primed with a NotI-oligo(dT) primer. Five prime end enritched, double-stranded CDNA was digested with Not I and cloned into the Not I and ECO RV sites of the pCMVSPORT 6 vector. Library was constructed by Life Technologies. Contact: Feng Liang Life Technologies, Contact: Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax: (1) 301 610 8371 Email: fliang@lifetech.com URL: http://fullength.invitrogen.com" 3 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="CSODF035YD19"
/clone_lib="LTI_F1013_FBrn1"
/dev_stage="pooled tissue from post conception fetuses (20 week, 24 week and 26 week)"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BQ178789 11.20354281 814 bp mRNA linear EST 30-APR-2002 UI-M-EV0-but-k-07-0-UI.rl NIH_BMAP_EV0 Mus musculus cDNA clone IMAGE:5701758 5', mRNA sequence. BQ178789 GI:20354281
information regarding entire library may be found at http://pga.swmed.edu/Data/Libraries/microarray_cdna_librar les.htm." 161 g 107 t
                                                                                                                                                                                                                                                                                                                                                                                                AL540071 LTL_FL013_FBrn1 Homo sapiens cDNA clone CSODF035YD19 5
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0
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1.5;
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1.6;
                                                                                                                                         1.6%; Score 23; DB
100.0%; Pred. No. 1.5
:Ive 0; Mismatches
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                                                                                                                                                                                                                                                             4 GAGCGCAACCGCATGCACAACCT 26
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AL540071
AL540071.1 GI:12869886
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BQ178789
LOCUS
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AL540071
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   /db_xref-"MGD:MGI:893591"
/translation-"MAPHPDALTIOVSPETQQPFPGASDHEVLSSNSTPPSHTLIPR
/translation-"MAPHPDALTIOVSPETALSKKRRSRRKKANDFERNRHHINSA
LDALKGVQPCFGTGRKTRARGGRRPPKSELALSKKRRSRRKKANDFERNRHHINSA
LDALKGVLPTFPDDAKLTKVETLRFAHNYIWALTQTLRIADHSLYGPEPPVPCGELGS
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2083-52 Mouse E14.5 retina lambda ZAP II Library Mus musculus CDNA,
mRNA sequence.
                                                                                                                        /sex="male"
/lssue_vppe="small intestine"
/clone_lib="RKEN full-length enriched mouse cDNA library"
/dev_stage="adult"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Cranlata; Vertebrata; Euteleostomi; Manmalia: Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 600)

Mu, X., Zhao, S., Pershad, R., Hsieh, T.-F., Scarpa, A., Wang, S.W., White, R.A., Beremand, P.D., Thomas, T.L., Gan, L., and Klein, W.H. Gene expression in the developing mouse retina by EST sequencing and microarray analysis

Nucleic Acids Res. 29 (24), 4983-4993 (2001)
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//dev_stage="mebryonic day 14.5 post-fertilization"
//note="Vector: pAMP10 (Gibco); Cloned unidirectionally.
Primer: Oilgo dT. RNA Isolation: cytoplasmic RNA preps
(Manniatis); Cloning Technique: CUA Cloning (CloneAmp,
Life Technologies); Average insert size: 1.8 Kb;
Insertion site: TACGTCCACTGAATTCTGAGTG--->. Other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PGGGSNGDWGSIYSPVSQAGNLSPTASLEEFPGLQVPSSPSYLLPGALVFSDFL"
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/clone_lib="Mouse E14.5 retina lambda ZAP II Library"
/tissue_type="neural retina"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       762 GCGCTGGATGCGCTGCCGGTGTCCTGCCCACCTTCCCGGATGACGCCAAACTTACAAAG 821
                                                                                                                                                                                                                                                                                                           /note="atonal homolog 5 (Drosophila)
data source:MGD, source key:MGI:893591, evidence:ISS
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4.1%; Score 60; DB 11; Length 1540;
Best Local Similarity 100.0%; Pred. No. 4.8e-20;
Matches 60; Conservative 0; Mismatches 0; Indels
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University of Texas M.D. Anderson Cancer Center
Box 117, 1515 Holcombe Blvd., Houston, Tx 77030, USA
Tel: 713 792 3646
Fax: 713 790 0329.
       /strain="C57BL/6J"
/db_xref="FANTOM_DB:2010001M19"
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                                                  /db_xref="MGD:MGI:1907403"
/db_xref="taxon:10090"
/clone="2010001M19"
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                                                                                                                                                                                                                                                                                                                                                                                                       /protein_id="BAB25411.1"
/db_xref="GI:12841942"
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                                                                                                                                                                                                                                                                                   /gene="Atoh5"
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241. .885
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Gaps

KEYWORDS SOURCE ORGANISM

REFERENCE AUTHORS TITLE JOURNAL COMMENT

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/note-"Vector: pBluescript II SK-; Site_1: EcoRI; Site_2:
XhoI; This library, constructed by John Davies and Jeffrey
McDermott, combines colbns from CC-1600 cells grown to
mid-log phase in TAP (acetate-containing) medium in the
light, TAP medium in the dark, HS (minimal) medium in
ambient levels of CO2 and HS medium bubbled with 5% CO2.
PolyA mRNA was purified from each sample, pooled and CDNA
synthesized. The CDNA was directionally cloned into lambda
ZAP II (Stratagene) in the EcoRI (5') and XhoI (3') sites.
pBluescript II SK-plasmids were excised from the lambda
ZAP clones by superinfection with ExAssist (Stratagene)
phage. The library was normalized using method 4 described
in Bonaldo et al (1996) Genome Research 6: 791-806."
Analyses of the Chlamydomonas reinhardtii Genome: A Model,
Unicellular System for Analyzing Gene Function and Regulation in
Vascular Plants: project phase 2
Unpublished (2000)
Contact: Charles Hauser
DCMB Box 91000
Duke University
Durham, Nc 27708-1000
Tel: 919 613 8159
Fax: 919 613 8177
Email: chauser@duke.edu.
Location/Qualifiers
1.1269
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone_lib="C. reinhardtii CC-1690, normalized, Lambda Zap
II"
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Eukaryota; Merazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

[ (bases 1 to 319)
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
Simpson,A.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Shotgun sequencing of the human transcriptome with ORF expressed
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1.6%; Score 23; DB 12; Length 1269;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 23; Conservative 0; Mismatches 0; Indels (
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                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Chlamydomonas reinhardtii"
/strain="CC-1690 wild type mt+ 21gr"
/db_xref="taxon:3055"
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Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
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AUTHORS
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/strain="GG7BL/6"
/db_xref="taxon:10090"
/clone="InAmap=5701758"
/clone="Inb="NIH_BMAP_EVO"
/tissue_type="who.b brain"
/dev_stage="embryo.15: 5 dpc"
/lab_host="blidg (T1 phage resistant)"
/note="Organ: brain; Vector: pYX-Asc; Site_1: BCOR I;
/note="Organ: brain; Vector: property of primer containing a Not I site. Double stranded conding of according to mRNA size fraction,
ligated with EcoR I adaptor, digested with Not I, and then cloned directionally into pYX-Asc vector. The library tag sequence located between the Not I site and the polyA tail
/ is GTGCGTGGAA. This library was created for the University of Iowa Mouse Brain Molecular Anatomy Project (BMAP); Gene Discovery in the Developing Mouse Nervous System', supported by National Instututes of Mental Health (NIMH), Hemin Chin, Ph.D., program coordinator:"

SITE_2 a 261 g 1102 t 2 others
                                                 Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutherla; Rodentia; Sciurognathi; Muridae; Murinae; Mus. C. 1 (bases 1 to 814)

National Institutes of Health, Mammalian Gene Collection (MCC)

National Institutes of Health, Mammalian Gene Collection (MCC)

National Institutes of Health, Mammalian Gene Collection (MCC)

Ontact: Robert Strausberg, Ph.D.
Email: ogapbs: Tefmall.nih.gov

Tissue Procurement: Dr. James Lin, University of Iowa CDNA Library preparation: Dr. M. Bento Soares, University of Iowa CDNA Library Prayed by: Dr. M. Bento Soares, University of Iowa DNA Sequencing by: Dr. M. Bento Soares, University of Iowa Clone Distribution: MGC clone distribution information can be http://image.llnl.gov

This clone was contributed by the Brain Molecular Anatomy Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BG854922 129-MAY-2001 1024041C06.y2 C. reinhardtii CC-1690, normalized, Lambda Zap II Chamydomonas reinhardtii cDNA, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chlamydomonas reinhardtii.
Chlamydomonas reinhardtii
Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
Chlamydomonadaceae; Chlamydomonas.
1 (bases 1 to 1269)
Grossman,A., Davies,J., Federspiel,N., Harris,E., Lefebvre,P.,
McDermott,J.P., Silflow,C., Stern,D. and Surzycki,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1.6%; Score 23; DB 14; Length 814;
100.0%; Pred. No. 1.6;
Live 0; Mismatches 0; Indels
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source

FEATURES

Query Match

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DEFINITION

RESULT 6 BG854922

ACCESSION

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REFERENCE AUTHORS

KEYWORDS SOURCE

BASE COUNT ORIGIN

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1 (Dases 1 to 464)

Mahairas, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T., Keller, A., Shaker, R., Furlong, J., Young, J.; Zhao, S., Adams, M.D. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AQ753599 464 bp DNA linear GSS 22-JUL-1999 HS_2117_A2_H03_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2117 Col=6 Row=0, DNA sequence.
                                                                                                                                                                                                                                    /note="Organ: nervous_tumor; Vector: puc18; Site_1: Smal; Site_2: Smal; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC18 vector. Reverse transcription of tissue mRNA and CDNA amplification were performed under low stringency conditions."
   This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=RC5-NT0053-310 800-034-E018453-2000-08-31&t4-1) seq primer: puc 18 forward forward forward High quality sequence stop: 319.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: jwallace@u.washington.edu
Clones may be purchased from Research Genetics (info@resgen.com).
BAC end web Server: http://www.htsc.washington.edu
Plate: 2117 row: 0 column: 6
Seq primer: M13 Reverse
Class: BAC ends
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="Organ: sperm; Vector: pBeloBAC11; BAC Clones in E-Coli DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999) 99380589
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0
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High Throughput Sequencing Center
University of Mashington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
TEL: (206) 616-3618
Eax: (206) 616-3887
                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 319;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
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Pred. No. 15;
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/organism="Homo sapiens"
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Location/Qualifiers
                                                                                                                                                                      /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="NT0053"
/dev_stage="Adult"
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Matches 21; Conserv
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AQ753599
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KEYWORDS
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ORIGIN

g δ

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/Jab_host="E. Coll strain XL10-Gold, Tl-resistant, P-"
/lab_host="E. Coll strain XL10-Gold, Tl-resistant, P-"
/lab_host="E. Coll strain XL10-Gold, Tl-resistant, M.
/note="Wector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jar.org/resources/documents/dnares/). The DNA
(http://www.jar.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
was blunt end repaired with T4 DNA polymerase and T4
was blunt end repaired with T4 DNA polymerase and T4
polymucleotide kinase. Adaptor oligonucleotides were
polymucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
ligated to the blunt ends in high molar excess. The
ligated to the blunt ends in high molar excess. The
ligated to the blunt ends in high was prepai
ligated to the blunt was purified and size-selected for a c-)
cells
electrophoresis. Vector DNA was prepai
inducible derivative of plasmid R1
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                                                                                                                                                                                                                                                                                                                                                                                                         A2506899 536 bp DNA linear GSS 05-OCT-2000 1M0348G13F Mouse 10kb plasmid UUGC1M library Mus musculus genomic close UUGC1M0348G13 F, DNA sequence.
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Busaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 536) mathor M neacorn.T.: Duval, B.; Hamil, C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly
, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.,
Manner, M., A., Malss, R.
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Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Fan. 308, Blomedical Polymers Research Bldg., 20 S. 2030 E., SLC
                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /strain="C57BL/6J"
/strain="C57BL/6J"
/clone="UUGC1M0348G13"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
                                                                                                                                           ö
                                                                                  Length 464;
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                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0348 row: G column: 13
Seq primer: CGTTGTAAAACGACGGCCAGT
                                                                                     DB 17;
16;
                                                                                                                                                     Mismatches
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123
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High quality sequence stop: 536.
                                                                                        Score 21;
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                                                                                                                                                                                                              492 CAAGTGTCCCAAGAGCCCAG 512
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Matches 21; Conservative 0
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Fax: 801 585 7177
Email: ddunn@genet
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Contact: Kobert Strandsberg, Ph.D.

Email: cgapbs r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
LLAMISIST STORES SOURCE SEQ.

S. Location/Qualifiers
S. Location/Qualifiers
S. Location/Qualifiers
S. Location/Qualifiers
S. Location/Qualifiers
S. Location-Lib-"Homo sapiens"
(Ab_xref-"taxon:9606"

/ Clone="IRAGE:5217154"

/ Clone="IRAGE:5217154"

/ Clone="IRAGE:5217154"

/ Lissue_type="leukocytes"

/ Lissue_type="leukocytes"

/ Lissue_type="leukocytes"

/ Lissue_type="leukocytes"

/ Lissue_type="leukocytes"

/ Lissue_type="leukocytes"

/ Library is normalized and enriched for cloning).

Research Genetics tracking code 027: Note: this is a NIH.MCC. Library.

/ Library is 166 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1.4%; Score 21; DB 13; Length 829;
100.0%; Pred. No. 18;
1ve 0; Mismatches 0; Indels
              1 (bases 1 to 829)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Coli.
                                                                                         Contact: Robert Strausberg, Ph.D.
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                                                                       Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 100.
Matches 21; Conservative
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BF204175
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                              AUTHORS
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/db_xref="taxon:9606"
/db_xref="taxon:9606"
/clone="INAGE:5537940"
/clone="INAGE:5537940"
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/lab_host="DH10B (phage-resistant)"
/note="Organ: lung; Vector: pOTB7; Site_1: Xhoi; Site_2: EcoR1; cDNA made by oligo-dT priming. Directionally cloned into EcoR1/Xhoi sites using the following?

RcoR1; cDNA made by oligo-dT priming. Directionally cloned into EcoR1/Xhoi sites using the following?

adaptor: GGACAGG(G). Size-selected by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript In RT (Life Technologies)."
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                                                                                                                                                                                                                                                                      BE263765
601194122F1 NIH_MGC_7 Homo sapiens cDNa clone IMAGE:3537940 5',
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                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
Bukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 718)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
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NIH-WGC http://mgc.nci.nih.gov/.
National institutes of Health, Mammalian Gene Collection (MGC)
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incytte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: LLCM996 row: a column: 07
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Email: cgapbs-rémail.nih.gov
Tissue Procurement: ATCC
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